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ACCESSION AR492934
VERSION AR492934.1 GI:47264085
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15186)
AUTHORS Peeters,B.P.H., de Leeuw,O.S. and Gielkens,A.L.J.
TITLE Newcastle disease virus infectious clones, vaccines and diagnostic assays
JOURNAL Patent: US 6719979-A 134 13-APR-2004;
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ACCESSION	AX008510
VERSION	AX008510.1 GI:9996061
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SOURCE	Newcastle disease virus
ORGANISM	Newcastle disease virus
REFERENCE	1
AUTHORS	Gielkens, A.L., Koch, G., De Leeuw, O. and Peeters, B.P.
TITLE	Newcastle disease virus infectious clones, vaccines and diagnostic assays
JOURNAL	Patent: WO 9966045-A 162 23-DEC-1999; GIELKENS ARNOUD LEONARD JOSEF (NL); KOCH GUUS (NL); LEEUW OLAV SVEN

DE (NL); PETERS BERNARDUS PETRUS HUBER (NL); STICHTING DIENST LANDBOUWKUNDI (NL)	FEATURES
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intron	14996. .15186		Db	5458	CTTATCCGTAAAGCAACACAGGGGATTTGCCCTCGGCACTTGTCCCCAAAAGTGGTGACACA	5517	
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	Matches 3355; Conservative 0; Mismatches 3; Indels 0; Gaps 0;		Db	5578	ATATTCTACAAGAAATAGTAACGTTCCCTATGTCCTCGTGTATTATTCTCTGCTTGACGG	5637	
Qy	1 ACGGTTAGAGATCTGGATCCCGTTCGGCCCTCCAGTGCAAGATGGGCTCGAGCC		Qy	1141	CAATACGTGGCCCTGTATGTACTCTCAAGAGACCGAAGGCGCACTTTACTACACCATATGAC	1200	

Db 5638 CAATACGTGGCCTGTATGTACTCAAGA CCGAAGGCGCACTTACTACCATCATGAC 5697
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	Qy	481	ACAAAATGTCGCAACATCTCTCGACTTAAAGAGAGACATTCGCGCAACCAATGAGCTGT	540
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	Qy	541	GCATGAGGTCACTGACGGGATTAACGCACTAGCAGTGGGAGAGATGACAGAGTT	600
	Db	5038	GCATGAGGTCACTGACGGGATTAACGCACTAGCAGTGGGAGAGATGACAGAGTT	5097
	Qy	601	TGTTAATGACCAATTTAAATAAAAACAGCTCAGGAATTAGACTGCATCAAAAATTCACAGCA	660
	Db	5098	TGTTAATGACCAATTTAAATAAAAACAGCTCAGGAATTAGACTGCATCAAAAATTCACAGCA	5157
	Qy	661	AGTTGCTGAGAGCTCAACTGTAACCGAATTTGACTACAGTATTCGGAACACAAAT	720
	Db	5158	AGTTGCTGAGAGCTCAACTGTAACCGAATTTGACTACAGTATTCGGAACACAAAT	5217
	Qy	721	CACCTCACCTGCTTTAAACAAAGCTGACTTACAGGACATTTTCAATCTAGCTCTGTGAAA	780
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	Qy	781	TATGGATTAATTTGACTAAGTTAGGTGTAGGGAACCAATCAACTCAGCTCATTAATCGG	840
	Db	5278	TATGGATTAATTTGACTAAGTTAGGTGTAGGGAACCAATCAACTCAGCTCATTAATCGG	5337
	Qy	841	TAGCGGCTTAATCACCGGTAACCTTCTATACGACTCACAGACTCAACTCTTGGGTAT	900
	Db	5338	TAGCGGCTTAATCACCGGTAACCTTCTATACGACTCACAGACTCAACTCTTGGGTAT	5397
	Qy	901	ACAGGTAACTCTACCTTCAGTCGGGAACCTTAATATATATGCGTGCCACCTTCTGGAAC	960
	Db	5398	ACAGGTAACTCTACCTTCAGTCGGGAACCTTAATATATATGCGTGCCACCTTCTGGAAC	5457
	Qy	961	CTTATCCGTAAAGCAACCAAGGGGATTTGCTCGGACCTTGTCCCAAAAGTGTGTGACCA	1020
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	Db	5518	GGTCGGTCTGTGATAGAGAACTTGACACTCATACTGTATATAGAAACTGACTTAGATTT	5577
	Qy	1081	ATATTGTACAGAAATAGTAACTGCTCCCTATGCTCCCTGGTATTTATTTCTGCTTGACGG	1140
	Db	5578	ATATTGTACAGAAATAGTAACTGCTCCCTATGCTCCCTGGTATTTATTTCTGCTTGACGG	5637
	Qy	1141	CAATAGCTCGGCTGTATGTACTCAAAGACCGAAGGCGCACTTACTACACATACATGAC	1200
	Db	5638	CAATAGCTCGGCTGTATGTACTCAAAGACCGAAGGCGCACTTACTACACATACATGAC	5697
	Qy	1201	TATCAAAGGTTCACTCATCGCCAACTGCAAGATGACAAATGTAGATGTGTAAACCCCC	1260
	Db	5698	TATCAAAGGTTCACTCATCGCCAACTGCAAGATGACAAATGTAGATGTGTAAACCCCC	5757
	Qy	1261	GGGTATCATATCGCAAAACTATCGAGAGACCGGTGTCTCTAATAGATATAAACAATCATGCA	1320
	Db	5758	GGGTATCATATCGCAAAACTATCGAGAGACCGGTGTCTCTAATAGATATAAACAATCATGCA	5817
	Qy	1321	TGTTTTATCTTAGGGGGGATAAATTTAAGGCTCAGTGGGGAATTCGATGTAACTTATCA	1380
	Db	5818	TGTTTTATCTTAGGGGGGATAAATTTAAGGCTCAGTGGGGAATTCGATGTAACTTATCA	5877
	Qy	1381	GAAGAAATATCTCAATCAAGATTTCTCAAGTAAATAAACAAGGCAATCTTGATATCTCAAC	1440
	Db	5878	GAAGAAATATCTCAATCAAGATTTCTCAAGTAAATAAACAAGGCAATCTTGATATCTCAAC	5937
	Qy	1441	TGAGCTTTGGGAATGTCAAACAATCTCGATCAGTAACTTTTGAATAGTTAGAGGAAGCA	1500
	Db	5938	TGAGCTTTGGGAATGTCAAACAATCTCGATCAGTAACTTTTGAATAGTTAGAGGAAGCA	5997
	Qy	1501	CAGAAACTAGACAAAGTCAATGTCAAACCTGACTAGCACATCTGCTCTCTATTACCTATAT	1560
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ORIGIN

Query Match	99.98;	Score	3353.2;	DB	14;	Length	15186;
Best Local Similarity	99.98;	Pred.	No. 0;				
Matches	3355;	Conservative	0;	Mismatches	3;	Indels	0;
						Gaps	0;
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Db	4498	ACGGGTAGAAGATTCTGGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGAC	4557				
Qy	61	TTCTTACCAAGAACCCAGCACTATGATGCTGACTATCCGGGTTGCGCTGCGACTGAGTTG	120				
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Qy	121	CATCTGTCGCGCAACTCCATTGATGCGAGCGCTCTTTCGAGCTGCGAGAAATTTGGTTAC	180				
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Qy	181	AGGAGACAAAGCCCTCAACATATACACTCATCCAGACAGGATCAATCATAGTTAAGCT	240				
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Qy	241	CTTCCCGAATCTGCCAAGAGTAAGAGGAGATGTGCGAAAGCCCCCTTGGATGCATACAA	300				
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Qy	301	CAGGACATTCACCACTTTGCTACCCCTTGGTGACTCTATCCGTAGGATACAAAGATC	360				
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Qy	361	TGTGACTACATCTCGAGGGGGAGACAGGGCGCTTTATAGCGCCCAATTTAGCGGCTGT	420				
Db	4858	TGTGACTACATCTCGAGGGGGAGACAGGGCGCTTTATAGCGCCCAATTTAGCGGCTGT	4917				
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QY	1561	CGTTTTGACTATCATATCTCTTGTGTTTTGGTATATCTTAGCCTGATTCCTAGCATGCTACCT	1620
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QY	1621	AATGTACAAGCAAAAGCGGCAACAAAAACCTTATTATGCTTGGGAATTAATCTCTAGA	1680
Db	6118	AATGTACAAGCAAAAGCGGCAACAAAAAGCCTTATTATGCTTGGGAATTAATCTCTAGA	6177
QY	1681	TCAGATGAGACCACTACAAAATGTGAACACAGATCAGAAACGAAAGGTTTCCCTAATAG	1740
Db	6178	TCAGATGAGACCACTACAAAATGTGAACACAGATGAGAAACGAAAGGTTTCCCTAATAG	6237
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QY	1801	TGTAGATGACAAAGGACGATATACGGGTAGAACCGGTAAAGAGGCGCCCTCAATTCG	1860
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QY	2041	TCCTTTTATATAGCATGGGGCTAGCACACCTAGCGATCTTGTAGGCATACCGACTAG	2100
Db	6538	TCCTTTTATATAGCATGGGGCTAGCACACCTAGCGATCTTGTAGGCATACCGACTAG	6597
QY	2101	ATTTTCAGGCGAGAGAAAGATTACATCTACACTTGTGTTCCCAATCAAGATGTAGTAGAT	2160
Db	6598	ATTTTCAGGCGAGAGAAAGATTACATCTACACTTGTGTTCCCAATCAAGATGTAGTAGAT	6657
QY	2161	AGGATATATAAGCAAGTGGCCCTTGAGTCTCCGTTGCGATTGTTAAATCTGAGACACA	2220
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QY	2221	ATTATGAACGCAATACATCTCTCTTATCAGATTAATGGAGCTGCAACACAGTGG	2280
Db	6718	ATTATGAACGCAATACATCTCTCTTATCAGATTAATGGAGCTGCAACACAGTGG	6777
QY	2281	TGGGGGCGACCTATCCATGACCCAGATTATATAGGGGGATAGGCAAGAACTCATTGTA	2340
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QY	2341	GATGATGCTAGTGATGTCACATCATCTATCCCTCTGCAATTCAGAAACATCTGAATTT	2400
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QY	3241	ACATTCAAATGCCCTCACTCGGCAGGTAGTATCCCTTGGCAGGCTTCAGCAAGATCCCC	3300
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RESULT 5

NDV18898

LOCUS

Newcastle disease virus cdNA to complete genomic RNA, clone 30.

DEFINITION

Y18898

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

1

Romer-Oberdorfer, A., Mundt, E., Mebatsion, T., Buchholz, U. J. and

Mettenleiter, T. C.

Generation of recombinant lentogenic Newcastle disease virus from

CDNA

J. Gen. Virol. 80 (Pt 11), 2987-2995 (1999)

20047980

10580061

2 (bases 1 to 15186)

Romer-Oberdorfer, A.

Direct Submission

JOURNAL	Submitted (31-MAR-1999) A. Roemer-Oberdoerfer, Federal Research	mRNA	4498. .6279
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ORIGIN

Query Match 99.98; Score 3353.2; DB 14; Length 15186;
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RESULT 6
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LOCUS Newcastle disease virus strain HB92 isolate V4, complete genome.
DEFINITION
ACCESSION AY225110
VERSION AY225110.1 GI:28824865
SOURCE
ORGANISM Newcastle disease virus
Newcastle disease virus
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Avulavirus.
REFERENCE 1 (bases 1 to 15186)
AUTHORS Pan, Z.S., Chen, Y.D., Shao, H.B., Yang, J., Xiong, Z.L., Wen, G.Y. and Zhang, C.Y.
TITLE Complete sequence for HB92 strain of Newcastle disease virus
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 15186)
AUTHORS Pan, Z.S., Chen, Y.D., Wen, G.Y. and Zhang, C.Y.
TITLE Direct Submission
JOURNAL Submitted (23-JAN-2003) Institute of Virology, Department of Life Science, Wuhan University, Wuhan, Hubei 430072, China
REFERENCE 3 (bases 1 to 15186)
AUTHORS Shao, H.B., Yang, J. and Xiong, Z.L.
TITLE Direct Submission
JOURNAL Submitted (23-JAN-2003) Institute of Animal Husbandry and Veterinary Science, Hubei Academy of Agricultural Science, Wuhan, Hubei 430209, China
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Qy	3301	AATCTGGTCTTACTGAGTCTATACAGATCCATATCCCTTATCTTATAGAAACC	3358
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RESULT 7
AF375823 LOCUS AF375823 15186 bp RNA linear VRL 06-NOV-2001
DEFINITION Newcastle disease virus strain B1 isolate Takaaki, complete genome.
ACCESSION AF375823

AF375823.1	GI:14190062	Newcastle disease virus B1
KEYWORDS		Newcastle disease virus B1
SOURCE		Viruses; ssRNA negative-strand viruses; Mononegavirales; Paramyxoviridae; Paramyxovirinae; Avulavirus.
ORGANISM		1 (bases 1 to 15186)
REFERENCE		Nakaya,T., Crois,J., Park,M.S., Nakaya,Y., Zheng,H., Sagrera,A., Villar,E., Garcia-Sastre,A. and Palese,P.
AUTHORS		Recombinant Newcastle disease virus as a vaccine vector
TITLE		J. Virol. 75 (23), 11868-11873 (2001)
JOURNAL		21548317
MEDLINE		11689668
PUBMED		Nakaya,T., Garcia-Sastre,A. and Palese,P.
REFERENCE		2 (bases 1 to 15186)
AUTHORS		Direct Submission
TITLE		Submitted (02-MAY-2001) Microbiology, Mount Sinai School of
JOURNAL		Medicine, One Gustave Levy Place, New York, NY 10029, USA
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DEFINITION	Newcastle disease virus B1, complete genome.		
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SOURCE	Newcastle disease virus B1		
ORGANISM	Newcastle disease virus B1		
REFERENCE	Paramyxoviridae; Paramyxovirinae; Avulavirus.		
AUTHORS	1 (bases 1 to 15186)		
TITLE	Sellers, H. S. and Seal, B. S.		
JOURNAL	Complete sequence for the B1 strain of Newcastle disease virus		
REFERENCE	2 (bases 1 to 15186)		
AUTHORS	Sellers, H. S. and Seal, B. S.		
TITLE	Direct Submission		
JOURNAL	Submitted (28-SEP-2000) U.S. Department of Agriculture/Agriculture		
FEATURES	Research Services, Southeast Poultry Research Laboratory, 934		
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ORIGIN

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RESULT 9
AY289002
LOCUS
DEFINITION
ACCESSION

AY289002
Newcastle disease virus turkey/USA/VGGA/89 fusion protein and
hemagglutinin-neuraminidase bicistronic mRNA, complete cds.
AY289002

3819 bp mRNA linear VRL 04-OCT-2004

AY289002.1	GI:3772483	
KEYWORDS	Newcastle disease virus	
SOURCE	Newcastle disease virus	
ORGANISM	Viruses; ssRNA negative-strand viruses; Mononegavirales; Paramyxoviridae; Paramyxovirinae; Avulavirus.	
REFERENCE	1 (bases 1 to 3819)	
AUTHORS	Seal,B.S.	
TITLE	Nucleotide and predicted amino acid sequence analysis of the fusion protein and hemagglutinin-neuraminidase protein genes among Newcastle disease virus isolates. Phylogenetic relationships among the Paramyxovirinae based on attachment glycoprotein sequences	
JOURNAL	Funct. Integr. Genomics 4 (4), 246-257 (2004)	
PUBLISHED	15108051	
REFERENCE	2 (bases 1 to 3819)	
AUTHORS	Seal,B.S.	
TITLE	Direct Submission	
JOURNAL	Submitted (01-WAY-2003) Agricultural Research Service, USDA, Southeast Poultry Research Laboratory, 934 College Station Road, Athens, GA 30605, USA	
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Best Local Similarity	98.6%;	Pred. No. 0;
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ORIGIN

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RESULT 10

A03663

LOCUS

DEFINITION Newcastle disease virus HN and F genes.

3825 bp

DNA

linear

PAT 13-DEC-1993

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QY 2581 ACTCTGGTTTCCATCAACCTGGACGACACCCCAAAATCGGAAGTCTTTCAGTGTGAGTGCA 2640
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ACCESSION	A03663
VERSION	A03663.1
KEYWORDS	GI:492839
SOURCE	.
ORGANISM	Newcastle disease virus Viruses; sRNA negative-strand viruses; Mononegavirales; Paramyxoviridae; Paramyxovirinae; Avulavirus. 1 (bases 1 to 3825)
REFERENCE	Bingham,R.W., Chambers,P., Emmerson,P.T. and Millar,N.S.
AUTHORS	Newcastle disease virus gene clones
TITLE	Patent: EP 0227414-A 2 01-JUL-1987:
JOURNAL	NATIONAL RESEARCH DEVELOPMENT CORPORATION
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Best Local Similarity	97.1%; Pred. No. 0;
Matches 3259; Conservative	0; Mismatches 99; Indels 0; Gaps 0;
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Dd	1 ACGGGTAGAGATTCTGGATCCCGGTTGGCGCCTTCTAGGTGCAAGATGGGCCACACC 60
Qy	61 TTCTACCAAGAACCCAGACTATGATGCTGACTATCCGGGTTGCGGCTGGCACTGAGTTG 120
Dd	61 TTCTACCAAGAACCCAGACTATGATGCTGACTGTCGAGTCCGGCTGGTACTGAGTTG 120
Qy	121 CATCTGTCGGCAAACTCCAATTGATGGCAGCCCTTTTGCAGCTGCAGGAATTGTGGTTAC 180
Dd	121 CATCTGTCGGCAAACTCCAATTGATGCAGSCCTCTTGCGCTSCAGGAATTGTGGTAAC 180

Qy	181	AGAGACAAAGCCGTC	CAATATACACCTCATCCGACAGAGGATCAATCACTAGTTAAGCT	240
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Qy	241	CCTCCGGAATCTGCC	CAAGGATAAGGAGGCATGTGCGAAAGCCCTTTGGATGCATACAA	300
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Qy	301	CAGGACATTGAC	CACTTTGTCTACCCCTCTTGTGACTCTATCCGTAGGATACAAGATGC	360
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Db	361	TGTAACTACATCTG	AGGGGGAGAGACAGAAACGCTTTATAGGCGCCATTATTGGCGGTGT	420
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Qy	481	ACAAATGCTG	CCAAACATCTCTCGACTTAAGAGAGCAATTCGCGCAACCAATGAGGCGGT	540
Db	481	ACAAATGCTG	CCCAACATCTCTCGACTTAAGAGAGCAATTCGCGCAACCAATGAGGCGGT	540
Qy	541	GCATGAGGTCACT	GACGGATTATTCGAACTAGCAGATGGCGAGTTGGGAAGATGACGACGATT	600
Db	541	GCATGAGGTCACTGACGATTATTCGAACTAGCAGATGGCGAGTTGGGAAGATGACGACGATT	600	
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Db	661	AGTTGGTTAGAGCTCAACCTGTACTTAA	CCGAAATGACTACAGTATTCGGACCAACAAT	720
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Qy	781	TATGGAATTA	CTTATGTAGCTAAGTTAGGTGATGGGAACAATCAACTCAGCTCATTAATCGG	840
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Qy	901	ACAGGTAAC	CTCTACCTTCAGTTCGGGAACCTTAATAATATGCGTGCCACCTACTTTGGAAC	960
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Qy	1021	GGTCGGTCTCTGTATAG	AAACTTGAACCTCATCTGTATAGAACTGACTTAGATTT	1080
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Qy	1081	ATAATTGTA	CAAGAAATAGTAACGTTTCCCTATGTCCCTCTGGTATTTATTTCTCTGCTTGAGCGG	1140
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Qy	1201	TATCAAAAGGTT	CAGTCAATCGCCAACTGCAAGATGACAAACATGTAGATGTGTAAACCCCCC	1260
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RESULT 11
E01252
LOCUS
DEFINITION Synthetic DNA encoding Newcastle disease virus (NDV) protein.
ACCESSION E01252

E01252 3825 bp DNA linear PAT 29-SEP-1997

VERSION	E01252.1	GI:2169511	
KEYWORDS	JP 1987163693-A/1.		
SOURCE	synthetic construct		
ORGANISM	synthetic construct		
REFERENCE	1 (bases 1 to 3825)		
AUTHORS	Richiyaado,U.B., Fuiritsupu,C., Piitaa,T.E. and Neiru,S.M.		
TITLE	NEWCASTLE DISEASE VIRUS GENE CLONE		
JOURNAL	Patent: JP 1987163693-A 1 20-JUL-1987;		
COMMENT	NATL RES DEV CORP		
	OS Artificial gene		
	OC Artificial sequence; Genes.		
	OS Newcastle disease virus (NDV)		
	PN JP 1987163693-A/1		
	PD 20-JUL-1987		
	PF 18-DEC-1986 JP 1986302719		
	PR 18-DEC-1985 GB 85 8531147, 14-APR-1986 GB 86 8609037, PR		
	15-JUL-1986 US 86 885765		
	PI RICHIIAADO UOOKAA BINGAMU, FUIRITSUPU CHIYANBAZU, PI PIITAA		
	TANREI EMAASON.		
	PI NEIRU SUTERYUWAATO MIRAA		
	PC C12N15/00,C12N1/20/A61K39/17,C12P21/02,C12N1/20,C12R1.19;		
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	CC topology: Linear;		
	CC hypothetical: No;		
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Best Local Similarity	97.0%;	Pred. No. 0;	
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QY	61	TTCTACCAAGAACCCAGCACTATGATGCTGACTATCCGGGTTGCGCTGGCACTGAGTTG	120
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QY	121	CATCTGTCCGGGAACTCCATTTGATGGAGGCGCTTTGCGAGCTGCGAGGAATTTGGTTAC	180
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Db	961	CTTATCTGTAAGCAACAACAGGGGATTTGCTGCGGCACTTTGTGCCAAAAGTGGTGCACAC	1020
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Db	1261	GGGTATCATATCGCAAACTATGGGAAGCCGCTGCTCTAAATAGATAAACAATCATGCAA	1320
QY	1321	TGTTTATCTTTAGCGGGATTAATTAAGGCTCAGTGGGGAATTCGATGTAATCTTATCA	1380
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RESULT 12

AY289000

LOCUS

DEFINITION

Accession

Version

Keywords

Source

Organism

Reference

Authors

Title

AY289000 4552 bp mRNA linear VRL 04-OCT-2004
Newcastle disease virus chicken/USA/Roakin/48 fusion protein and
hemagglutinin-neuraminidase bicistronic mRNA, complete cds.
AY289000
AY289000.1 GI:33772477
Newcastle disease virus
Newcastle disease virus
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Avulavirus.
Seal, B.S.
Nucleotide and predicted amino acid sequence analysis of the fusion
protein and hemagglutinin-neuraminidase protein genes among
Newcastle disease virus isolates. Phylogenetic relationships among
the Paramyxovirinae based on attachment glycoprotein sequences

JOURNAL	Funct. Integr. Genomics 4 (4), 246-257 (2004)	Db	301	CAGGACATTGACACACTTTGCTCACCCCCCTTGGTGACTCTATCCGCTAGGATACAAGAGTC	360
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REFERENCE	2 (bases 1 to 4552)	Db	361	TGTAACTACATCTGGAGGGAGGAGCAGAAAAGCTTTATAGGGCCATTTATTGGCGGTGT	420
AUTHORS	Seal, B-S	Qy	421	GGCTCTTGGGGTGGCAACTGGCCGCAAAATAACAGCGCGCGGAGCTTCTGATACAAAGCCAA	480
TITLE	Submitted (01-MAY-2003) Agricultural Research Service, USDA, Southeast Poultry Research Laboratory, 934 College Station Road, Athens, GA 30605, USA	Db	421	GGCTCTTGGGGTGGCAACTGGCTGCAAAATAACAGCGCGCGGAGCTTCTGATACAAAGCCAA	480
JOURNAL		Qy	481	ACAAATGCTGCGCAACATCTCCGACTTAAAGAGAGCATTTGGCGCAACCAATGAGGCCGT	540
FEATURES		Db	481	ACAAATGCTGCGCAACATCTCCGACTTAAAGAGAGCATTTGGCGCAACCAATGAGGCCGT	540
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	KNDGVREARSG"	Qy			
		Db			
ORIGIN		Qy			
Query Match	95.0%; Score 3190; DB 14; Length 4552;	Db			
Best Local Similarity	96.9%; Pred. No. 0;	Qy			
Matches 3253; Conservative	0; Mismatches 105; Indels 0; Gaps 0;	Db			
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Qy	301	CAGGACATTGACCACTTGTCTACCCCCCTTGGTGACTCTATCCGTAGGATACAAGAGTC	360		

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Qy	1561	CGTTTTGACTATCATATCTCTTGTTTTGGTATATCTTAGCCTGATTTAGCATGCTACCT	1620
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RESULT 13

NDVFNH	3825 bp	RNA	linear	VRL 09-JAN-1998
LOCUS	Newcastle disease virus gene for fusion glycoprotein precursor,			
DEFINITION	haemagglutinin-neuraminidase glycoprotein precursor.			
ACCESSION	D00243			
VERSION	D00243.1	GI:22174		
KEYWORDS	haemagglutinin-neuraminidase glycoprotein precursor; fusion glycoprotein precursor; F; HN; NDV; avirulent.			
SOURCE	Newcastle disease virus			
ORGANISM	Viruses; ssRNA negative-strand viruses; Mononegavirales; Paramyxoviridae; Paramyxovirinae; Avulavirus.			
REFERENCE	1 (bases 1 to 3825)			
AUTHORS	Millar, N.S., Chambers, P. and Emerson, P.T.			
TITLE	Nucleotide sequence of the fusion and haemagglutinin-neuraminidase			

glycoprotein genes of Newcastle disease virus, strain Ulster:
molecular basis for variations in pathogenicity between strains
J. Gen. Virol. 69 (Pt 3), 613-620 (1988)
88171450
3351479
PUBMED

COMMENT

TO understand the molecular basis for the differences in virulence
shown by strains of NDV, the sequences of the E and HN genes of the
extremely avirulent strain Ulster were determined and compared with
those of several other NDV strains (discussed in [1]).

FEATURES

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3816. .3825

ORIGIN

Query Match 84.2%; Score 2826.8; DB 14; Length 3825;
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Matches 3026; Conservative 0; Mismatches 332; Indels 0; Gaps 0;

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RESULT 14
AY562991
LOCUS
DEFINITION

AY562991 15186 bp RNA linear VRL 22-MAR-2004
Newcastle disease virus isolate chicken/N. Ireland/ulster/67,
complete genome.

ACCESSION AY562991
VERSION AY562991.1 GI:45511246
SOURCE Newcastle disease virus
ORGANISM Newcastle disease virus
REFERENCE 1 Viruses; ssRNA negative-strand viruses; Mononegavirales; Paramyxoviridae; Paramyxovirinae; Avulavirus.
AUTHORS 1 (bases 1 to 15186)
Wise, M.G., Kuntz, R.L. and Seal, B.S.
TITLE Comparison of full-length genome sequences among the Paramyxoviridae
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 15186)
Wise, M.G., Kuntz, R.L. and Seal, B.S.
AUTHORS Direct Submission
TITLE Submitted (01-MAR-2004) Southeast Poultry Research Laboratory, U.S. Dept. of Agriculture, ARS, 934 College Station Rd., Athens, GA 30605, USA
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ORIGIN

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Matches 3021;		Conservative 0;	Mismatches 337;	Indels 0;	Gaps 0;
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LOCUS   Newcastle disease virus strain Herts/33, complete genome. 15186 bp RNA linear VRL 06-OCT-2004
ACCESSION AY741404
VERSION   AY741404.1 GI:53636432
KEYWORDS  Newcastle disease virus
SOURCE    Newcastle disease virus
ORGANISM  Viruses; ssRNA negative-strand viruses; Mononegavirales;
           Paramyxoviridae; Paramyxovirinae; Avulavirus.
REFERENCE 1 (bases 1 to 15186)
AUTHORS   de Leeuw,O.S., Hartog,L., Ravenshorst,N., Koch,G. and
           Peeters,B.P.H.
TITLE      Virulence of Newcastle disease virus is determined by the cleavage
           site of the fusion protein and both the stem region and globular
           head of the hemagglutinin-neuraminidase protein
JOURNAL    Unpublished
REFERENCE 2 (bases 1 to 15186)
AUTHORS   de Leeuw,O.S. and Peeters,B.P.H.
TITLE      Direct Submission
JOURNAL    Submitted (03-SEP-2004) Infectious Diseases, Wageningen University
           and Research Centre, Animal Sciences Group, Edelhertweg 15,
           Lelystad, Flevoland 8200 AB, The Netherlands
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LAKIAMSHPVKAALRASSVLIWAYGNEVNAALAKIARSCNISEYLRLLSPLEPT
AGNIHQRLDDQITQMTFTPASLYRVSPYTHISNDQRLFTEEGVKGNVYQIIMLIG
LSIIESLPMTTKTYDEITLHLHSKESCIREAPVAPPELLAGLAPELRAVTSNKFEM
YDPSPVSEGDFARLDLAIKPSYELNLESPTIELMNLISSSCKLIGQSVVSVDEDT
IKNDALIYDNTFARLISEAQNSDVRLFEYALEVLLDCSYQIYLRVGNINVLVIM
SDLYKNMPGILLISNIAATISHPIHSLRANAVGLNVHDSHQDLADTFIENSALVSC
TRRVVSGLYAGNRYDILLFPSLDNLSERMLQILSRCLCYTLVLTFAITREIPKIRGLS
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DITLALLFQPELLEPVSQDVGARVKDPTROPAAFLQELDLSAPARYDAFTLSQVH
SEHTLNPEEDILRVYLRFGITGATASSWYKASHLLSVPEVRCARHNSLYLAGSGAI
MSLLELHUPHETIYNTLPSNENPPORHFGPTPTQLNSVYVRNQAQVPCDGPVQ
EFHPLWRENTESDLTSDKAVGITSAPYRSVSLHCDIEIPPSNQSLLDOLATNL
SLTIAMHSVREGGVIIKVIYMGYVPHLLMNLFPAGCTGTGYILNSGACRGMDECYLI
FYWYLGPGTFVHEVVRMAKTLVRRHGTLLSKSDEITLTRLFTSQOHRVTDLILSSPLP
RLMKFLRENIDALIEAGQVPRPFCAESLVTLKDMOTOMTOIIASHIDTVIRSVIYM
EABGDLDLVLFTPTPNLSDGKKRSLAQCTQIILEVITLGLRAKDLNKKVGVIGILV
LGRMISLELDILPLRTLYLKRSTCPKYLKAVLIGITKLEMFDTTSLLYLTRAQQKPYMKT
IGNAAKGYYSNDNS"
ORIGIN
Query Match 80.3%; Score 2695.6; DB 14; Length 15186;
Best Local Similarity 87.7%; Pred. No. 0;
Matches 2944; Conservative 0; Mismatches 414; Indels 0; Gaps 0;
QY 1 ACGGGTAGAAGATCTTGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACC 60
|||||
Db 4498 ACGGGTAGAAGATTTGGATCCCGGTTGGACATTCAGGTGCAAGATGGGCTCCAGATC 4557
|||||
QY 61 TTCTACCAAGAACCCAGCACTATGATGCTGACTATCCCGGTTGCGCTGGCACTGAGTTG 120
|||||
Db 4558 TTCTACCAAGATCCCGGTTCTCCAATGCTGATCATCCGAATTTGCTGACGCTGAGTTG 4617
|||||
QY 121 CATCTGTCGGGAAACTCCATTCATGTCAGGAGCCTCTTGACGCTGCAGGAATTTGGTTAC 180
|||||

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Db	4618	TATCCGCTCTGCAAGCTCTCTTGATGGCAGGCCCTCTTGAGCTGCGAGGATCGTGGTAAC	4677
QY	181	AGGAGACAAAGCCGTCACATATATACACCTCATCCACAGACAGGATCAATCATAGTTAAGCT	240
Db	4678	AGGATTAAGCAGTCAACATATATACACCTCATCCAGACAGGCTCAATCATAGTCAAGTT	4737
QY	241	CTCCCGAATCTGCCAAGGATGAAGGAGGATGTGGGAAAGCCCCCTTGGATGCATACAA	300
Db	4738	ACTCCCAAAATATGCCAAGGACAAAGAGGGGTGTGCAAAAGCCCCATTTGGAGGCATACAA	4797
QY	301	CAGGACATTCAGCACCTTTGTCTACCCCTTGTGTGACTCTATCCGTAGGATACAGAGTC	360
Db	4798	CAGGACATGACTACTTTGTCTACCCCTTGTGTGACTCTATCCGTAGGATACAGAGTC	4857
QY	361	TGTGACTACATCTGGAGGGGGGAGACAGGGCGCCCTTATAGGCGCAATTTATTCGGCGGTGT	420
Db	4858	TGTGACTACTTCCGGAGGAGGAGACAGAGCCCTTTATAGGTGCCATTTATTCGGCAGTGT	4917
QY	421	GGCTCTTTGGGGTTGCCAATCTGCCGCACAAAATAACAGCGGGCCGCAAGCTCTGTATACAAGCCAA	480
Db	4918	AGCTCTTTGGGGTTGCCAAGCTGCACAGATAACCGGACGCTCGGCCCTGTATACAAGCCAA	4977
QY	481	ACAAATGTCTGCCAACAATCTCCGACTTAAAGAGAGCATTTGCCGGAACCAATGAGGCTGT	540
Db	4978	CCAGAAATGTCTGCCAACAATCTCCGCTTAAAGAGAGCATTTGTCTGCAACCAATGAAGCTGT	5037
QY	541	GCATGAGTCACTGACGGATTATCGCAACTAGCAGTGGCAGTTGGGAAGATGACAGCTT	600
Db	5038	GCAGAGGTCACTGACGGATTATCAACATAGCAGTGGCAGTAGGGAAGATGACAGCTT	5097
QY	601	TGTTAATGACCAATTTAATAAAACAGCTCAGGAATTAGACTGCATCAAAATTTGCACAGCA	660
Db	5098	TGTTAATGACCAATTTAATAACAGCGCAAGATTTGGACTGTATTAATAATTTACACAGCA	5157
QY	661	AGTTGGTGTAGACTCAACTGTACTTAACCGAATTTGACTACAGTATTTGGACCACAAT	720
Db	5158	GGTAGGTGTAGAACTCAACTGTACTTAACCGAATTTGACTACAGTATTTGGGGCACAAAT	5217
QY	721	CACCTCACCTGCTTTAAACAAGCTGACTATTTAGGCACTTTACAATCTAGCTGCTGGAA	780
Db	5218	CACCTCCCTGCTTTAACTCAGCTGACTATTCAGGGCGCTTTACAATTTAGCTGGTGTAA	5277
QY	781	TATGGAATTAATTTGACTAAGTTAGGTGTAGGGAACAATCAACTCAGCTCATTAATTCGG	840
Db	5278	TATGGAATTAATTTGACTAAGTTAGGTGTAGGGAACAATCAACTCAGCTCATTAATTCGG	5337
QY	841	TAGCGGCTTAATCAGCGGTAAACCTTATCTATAGGACTACAGACTCAACTCTTTGGGTAT	900
Db	5338	TAGCGGCTTGATCAGCGGCAACCTTATCTGTACGACTCACAGACTCAGACTCTTTGGGTAT	5397
QY	901	ACAGGTAACCTTACCTTCAGTCGGGAACCTTAATAATATATGCGTGCCACCTTCTTGGAAAC	960
Db	5398	ACAGGTAACCTTTCCTTCAGTCGGGAACCTTAATAATATATGCGTGCCACCTTCTTGGAGAC	5457
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Db	5458	CTTATCTGTAAAGCACACACAGGGATTTGCTCGGCACCTTTGCCAAAAGTGGTGACACA	5517
QY	1021	GGTCGGTCTGTGATAGAAGAACTTGACACCTCATCTGTGATAGAAGCTTGTAGATT	1080
Db	5518	GGTCGGTCTGTGATAGAAGAACTTGACACCTCATCTGTGATAGAAGCTTGTAGATT	5577
QY	1081	ATAATTCGACAGAAATAGTAACTTCCCTATGCTCCCTGGTATTTATTCCTGCTTGAACGG	1140
Db	5578	ATACTGTACAGAAATAGTAACTTCCCTATGCTCCCTGGTATTTATTCCTGCTTGAACGG	5637
QY	1141	CAATAGCTCGCCCTGTATGTACTCAAGAACCGAAGCGCACTTACTACACCATACATGAC	1200
Db	5638	TATACATCGCTTGTATGTATCAAGACTGAAGCGCACTTACTACGCCATATATGCG	5697
QY	1201	TATCAAGAGTTGATGATCGCCAACTGCAAGATGACAAATGTAGATGTGTAAACCCGCC	1260
Db	5698	TCTCAAGAGGCTCAGTTATTGCAATTTGCAAGATGACAAATGTAGATGTGTAGATGTGTGTA	5757

QY	1261	GGGTATCATATCGCAAAACTATGGAGAGCCGTGTCTCTAATAGATAAAACAATCATGCA	1320
Db	5758	GGGTATCATATCGCAAAACTATGGAGAGCTGTGTCTTAAATAGATAGGCACTCATGCAA	5817
QY	1321	TGTTTATCTCTAGCGGGATAACTTTAAGGCTCAGTGGGGAATTCGATGTAACTTATCA	1380
Db	5818	TGTTTATCTCTAGCGGGATAACTCTGAGGCTCAGTGGGGAATTTGATGCAACCTTATCA	5877
QY	1381	GAAGATATCTCAATACAGATTTCTCAAGTAAATAACAGGCAATCTTGATATCTCAAC	1440
Db	5878	AAAGATATCTCAATACAGTATCTCAAGTATAGTGACAGGCAATCTCGATATATCAAC	5937
QY	1441	TGAGCTTTGGGAATGTCAACAACTCGATCAGTAAATGCTTTGAAATAAGCTTAGAGGAAAGCAA	1500
Db	5938	TGAGCTTTGGGAATGTCAACAACTCANTAAATAGTAAATGCTTGAAGTAACTTAGAGGAAAGCAA	5997
QY	1501	CAGAAACTAGACAAAGTCAATGTCAAACTAGCACTAGCACTCTCTCTCATTTACCTATAT	1560
Db	5998	CAGAAACTAGACAAAGTCAATGTCAAGCTGACCAAGCACTCTCTCTCATTTACTTACAT	6057
QY	1561	CGTTTGTACTATCATATCTCTTGTGTTTGGTATCTAGCTGATTTCTAGCATGCTACCT	1620
Db	6058	CGTTTAACTGTATATCTCTTGTGTTTGGTGTACTTAGCTGGTTCTTAGCATGCTACCT	6117
QY	1621	AATGTACAAAGCAAAAGCGCAACAAAAACCTTATTTATGCTTGGGAAATAATACTCTAGA	1680
Db	6118	GATGTACAAAGCAAAAGCGCAACAAAAACCTTATTTATGCTTGGGAAATAATACTCTAGA	6177
QY	1681	TCAGATGAGAGCCACTACAAAAATGTGAACAGATGAGGAACGAAAGGTTTCCCTAATAG	1740
Db	6178	TCAGATGAGAGCCACTACAAAAATGTGAACAGATGAGGAACGAAAGGTTTCCCTAATAG	6237
QY	1741	TAATTTGTGTGAAGTTCTTGGTGTCTGTCTGCTCAGAGAGTTTAAGAAAAAAGCTA	1800
Db	6238	CAATTTGCTGTGAAGTTCTTGGTGTCTGTCTGCTCAGAGAGTTTAAGAAAAAAGCTA	6297
QY	1801	TGTAGATGACCAAAAGGACGATATACGGGTAGAACCGGTAAAGAGAGGCGCCCTCAATTCG	1860
Db	6298	TGTAGTGTACAAAAAGCAATACAGGCTAGAACCGGTGCGGGAAGCACTCCCTCAATTCG	6357
QY	1861	GAGCCAGGCTTCAACACCTCCGTTCTACCGTTACCGCAACACAGTCTCAATCATGGAC	1920
Db	6358	GAATCAGGCTCTCATACGCTCTTCTACCGCATCAACATAGCAAACTTCGGTTATGGAC	6417
QY	1921	CGGCGGTTAGCCAGTTGGGTTAGGAATGATGAAGAGAGGCAAAAAATACATGGCGC	1980
Db	6418	CGTGCAGTTAGCAGAGTTGCGCTTAGAGAAATGAAGAAAGAGAAAGAAATACATGGCGC	6477
QY	1981	TTGATATTCGGATTCGAATCTTATTTCTTAAACAGTAGTAGACCTTGCTGTATATCTGTAGCC	2040
Db	6478	TTTGTATTCGGATTCGAATCTTATTTTAAATAGTAAATACCTTAGCCATCTCTGAGCC	6537
QY	2041	TCCTTTTATATAGCATGGGGCTAGCACACCTTAGCGATCTTGTAGGCATACCGACTAGG	2100
Db	6538	GCCCTGGTATATAGCATGGAGCTAGCACGCGGGGCACTTGTGGCATACCAACTGTG	6597
QY	2101	ATTTCCAGGGCAGAGAAAAAGATTACATCTACCTTGGTTCCCAATCAAGATGTAGTAGAT	2160
Db	6598	ATCTCTAGGGCAGAGAAAAAGATTACATCTGACCTCAGTTCTTAATCAAGATGTAGTAGAT	6657
QY	2161	AGGATATATAAGCAAGTGGCCCTTGGTGTCTCGTTGGCATCTGTTAAATACTGAGACACA	2220
Db	6658	AGGATATATAAGCAAGTGGCCCTTGGTGTCTCGTTGGCATCTGTTAAATACTGAGACACA	6717
QY	2221	ATTAAGAACGCAATAACATCTCTCTTATCAGATTAATAGGAGCTGCAACCAACAGTGGG	2280
Db	6718	ATTAAGAACGCAATAACAGTCTCTCTCTTATCAATCAATGGAGCTGCAAAATATAGCGGG	6777
QY	2281	TGGGGGCACTTATCCATGACCCAGATTATATAGGGGGATAGGCAAGAACTCATTTGTA	2340
Db	6778	TGTGGGGCACTTATCCATGACCCAGATTATATAGGGGGATAGGCAAGAACTCATTTGTA	6837

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 1, 2005, 11:15:17 ; Search time 1694 Seconds
(without alignments)
11734.647 Million cell updates/sec

Title: US-10-800-256-1
Perfect score: 3358
Sequence: 1 acgggtagaagattctggat.....cctaattcttatagaacc 3358

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3358	100.0	3358	8 ACC47077	Acc47077 Nucleotid
2	3353.2	99.9	15186	3 RAZ44617	Aaz44617 Newcastle
3	3353.2	99.9	15186	10 ADH71088	Adh71088 Newcastle
4	3353.2	99.9	15186	10 ADH62844	Adh62844 Newcastle
5	3240.4	96.5	5292	12 ADM78414	Adm78414 Newcastle
6	3196.4	95.2	3825	1 AN70261	An70261 Sequence
7	2441.6	72.7	5291	12 ADM78418	Adm78418 Newcastle
8	1741.8	51.9	4177	2 AAQ68943	Aaq68943 Sfii frag
9	1741.8	51.9	4177	2 AAQ70570	Aaq70570 Sfii frag
10	1741.8	51.9	4177	2 AAT48510	Aat48510 Sfii frag
11	1741.8	51.9	4177	2 AAX81147	Aax81147 Seq ID No
12	1741.8	51.9	4177	3 AAZ49295	Aaz49295 CDNA enco
13	1741.8	51.9	4177	3 AAC67862	Aac67862 Sfii frag
14	1701.6	50.7	3570	6 ABK90556	Abk90556 Newcastle
15	1631.6	48.6	1662	2 AAT18203	Aat18203 Newcastle
16	1511	45.0	1907	2 AAQ98633	Aaq98633 Newcastle
17	1511	45.0	1907	2 ADH23624	Adh23624 Newcastle
18	1509.4	44.9	1907	2 AAQ46678	Aaq46678 NDV Haema
19	1448	43.1	2176	2 AAQ13668	Aaq13668 Newcastle
20	1427.2	42.5	1704	2 AAQ10060	Aaq10060 F gene of

21	1421.6	42.3	1734	2 AAT18205	Aat18205 Newcastle
22	1414.6	42.1	1812	4 AAC93148	Aac93148 Newcastle
23	1414	42.1	1662	12 ADP64628	Adp64628 DNA encod
24	1374.6	40.9	1685	6 AAL39864	Aal39864 DNA of F
25	1374.6	40.9	1685	10 ACC83258	Acc83258 Nucleotid
26	1368.4	40.8	2521	2 AAV42534	Aav42534 DNA encod
27	1368.4	40.8	2521	12 ADM41154	Adm41154 Nucleotid
28	1365.2	40.7	2521	2 AAT35875	Aat35875 Newcastle
29	1365.2	40.7	2521	2 AAT39330	Aat39330 Newcastle
30	1365.2	40.7	2521	2 AAT35921	Aat35921 Newcastle
31	1365.2	40.7	2521	2 AAV07021	Aav07021 Newcastle
32	1364	40.6	1734	2 AAT71745	Aat71745 Paramyxov
33	1362.8	40.6	1682	2 AAV49342	Aav49342 Newcastle
34	1354.8	40.3	1784	1 AAN81290	Aan81290 New recom
35	1353.2	40.3	1764	2 AAQ20794	Aaq20794 Newcastle
36	1290	38.4	1999	2 AAQ05549	Aaq05549 Sequence
37	1290	38.4	2000	1 AAN91000	Ana91000 Sequence
38	1238.2	36.9	1867	6 ABA99929	Aba99929 NDV HN DN
39	1196.8	35.6	1584	11 ADO55921	Ado55921 Newcastle
40	1193.6	35.5	1584	11 ADO55922	Ado55922 Newcastle
41	1192	35.5	1584	11 ADO55920	Ado55920 Newcastle
42	1160.8	34.6	1716	2 AAV49339	Aav49339 Newcastle
43	1090.4	32.5	1805	1 AAN91032	Ana91032 Haemagglu
44	1043.4	31.1	1648	11 ADO55933	Ado55933 Newcastle
45	1040.2	31.0	1648	11 ADO55936	Ado55936 Newcastle

ALIGNMENTS

RESULT 1
ACC47077
ID ACC47077 standard; DNA; 3358 BP.
XX
AC ACC47077;
XX
DT 23-JUN-2003 (first entry)
XX
DE Nucleotide sequence of F and HN genes of NDV strain HJ9.
XX
KW NDV; lentogenic; oncolytic; fusion glycoprotein; F gene; HN gene;
KW haemagglutinin-neuraminidase; cytotstatic; gene therapy; cancer; gene; ds.
XX
OS Newcastle disease virus.
XX
PH Key Location/Qualifiers
FT CDS 47..3358
FT /*tag= a
FT /note= "contains internal stop codons"
XX
PN WO2003022202-A2.
XX
PD 20-MAR-2003.
XX
PF 12-SEP-2002; 2002WO-IL000765.
XX
PR 12-SEP-2001; 2001IL-00145397.
XX
PA (YISS) YISSUM RES & DEV CO.
PA (OVCU-) OVCURE INC.
XX
PI Zakay-Rones Z, Panet A, Irving C;
XX
DR WPI; 2003-354498/33.
DR P-PSDB; ABR39678.
XX
PT Clonal lentogenic oncolytic strain, particularly a HJ9 strain, of
PT Newcastle Disease Virus, useful for treating cancer, comprises a DNA
PT encoding a fusion gene and/or a hemagglutinin-neuraminidase gene.
XX
PS Claim 1; Page 18-21; Sipp; English.
XX
CC The invention relates to a clonal lentogenic oncolytic strain of

CC Newcastle Disease Virus (NDV) comprising a DNA sequence encoding for the
CC fusion glycoprotein (F) gene and a part of the haemagglutinin-
CC neuraminidase (HN) gene. The lentogenic oncolytic strain of NDV or a
CC viral glycoprotein having oncolytic activity, is useful in preparing a
CC composition for the treatment of cancer. The present sequence represents
CC a NDV strain HUU nucleotide sequence containing all of the F gene, an
CC intergene and most of the HN gene
XX

SQ Sequence 3358 BP; 984 A; 785 C; 746 G; 843 T; 0 U; 0 Other;

Query Match 100.0%; Score 3358; DB 8; Length 3358;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3358; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ACGGGTAGAAGATTCTCGAATCCGGTTGGCGCCCTCCAGGTGCAAGATGGCTCCAGACC	60
DB	1	ACGGGTAGAAGATTCTCGAATCCGGTTGGCGCCCTCCAGGTGCAAGATGGCTCCAGACC	60
QY	61	TTCTACCAAGAACCCAGCACCTATGATGCTGACTATCCGGGTTGGCGTGGCACTGAGTTG	120
DB	61	TTCTACCAAGAACCCAGCACCTATGATGCTGACTATCCGGGTTGGCGTGGCACTGAGTTG	120
QY	121	CATCTGTCCGCGAAAATCCCAATGATGCGCAGGCTCTTGACAGTGCAGGAATGTTGGTTAC	180
DB	121	CATCTGTCCGCGAAAATCCCAATGATGCGCAGGCTCTTGACAGTGCAGGAATGTTGGTTAC	180
QY	181	AGGAGACAAAGCCGTCAACATATACACCTCATCCAGACAGGATCAATCATAGTTAAGCT	240
DB	181	AGGAGACAAAGCCGTCAACATATACACCTCATCCAGACAGGATCAATCATAGTTAAGCT	240
QY	241	CCTCCCGAATCTGCCAAGGATAAGGAGGATGTGCGAAAGCCCCCTTGGATCATACAA	300
DB	241	CCTCCCGAATCTGCCAAGGATAAGGAGGATGTGCGAAAGCCCCCTTGGATCATACAA	300
QY	301	CAGGACATTGACACATTTGCTCAACCCCTTGGTGAATCTATCCGTAGGATACAAGATC	360
DB	301	CAGGACATTGACACATTTGCTCAACCCCTTGGTGAATCTATCCGTAGGATACAAGATC	360
QY	361	TGTGACTACATCTGGAGGGGGAGACAGGGCGCCTTATAGGCGCCATTTATGGCGGTGT	420
DB	361	TGTGACTACATCTGGAGGGGGAGACAGGGCGCCTTATAGGCGCCATTTATGGCGGTGT	420
QY	421	GGCTCTTGGGTTGCCAATCTCCCGCACAAATTAACAGCGCGCGAGCTCTGTATACAAGCCAA	480
DB	421	GGCTCTTGGGTTGCCAATCTCCCGCACAAATTAACAGCGCGCGAGCTCTGTATACAAGCCAA	480
QY	481	ACAAATGCTGCCAATCTCCGACTTAAAGAGAGCATTTGCCGCAACCAATGAGGCTGT	540
DB	481	ACAAATGCTGCCAATCTCCGACTTAAAGAGAGCATTTGCCGCAACCAATGAGGCTGT	540
QY	541	GCATGAGTCACTGACGGATTATCGCACTAGCAGTGGCAGTTGGGAAGATGACGAGTT	600
DB	541	GCATGAGTCACTGACGGATTATCGCACTAGCAGTGGCAGTTGGGAAGATGACGAGTT	600
QY	601	TGTTAATGACCAATTTAATAAAGCAGCTCAGGAATTTAGACTGCATCAAAATTTGCACAGCA	660
DB	601	TGTTAATGACCAATTTAATAAAGCAGCTCAGGAATTTAGACTGCATCAAAATTTGCACAGCA	660
QY	661	AGTTGGTGTAGAGCTCAACCTGTACCTAACCGAATTTGACTACAGTATTCGGACCAAAAT	720
DB	661	AGTTGGTGTAGAGCTCAACCTGTACCTAACCGAATTTGACTACAGTATTCGGACCAAAAT	720
QY	721	CACCTTCACCTGCTTTAAACAAGCTGACTATTTAGGCACTTTTCAATCTAGCTGGTGA	780
DB	721	CACCTTCACCTGCTTTAAACAAGCTGACTATTTAGGCACTTTTCAATCTAGCTGGTGA	780
QY	781	TATGGATTACTTATGACTAAGTTAGGTGTAGGGAACAATCAACTCAGCTCATTAATCGG	840
DB	781	TATGGATTACTTATGACTAAGTTAGGTGTAGGGAACAATCAACTCAGCTCATTAATCGG	840
QY	841	TAGGGCTTAATCACCGGTAACCCCTATTCTATACGACTCACAGACTCAACTCTTGGGTAT	900
DB	841	TAGGGCTTAATCACCGGTAACCCCTATTCTATACGACTCACAGACTCAACTCTTGGGTAT	900

QY	901	ACAGGTAACTTACCTTCCAGTCGGGAACCTAAATAATATCGTGCACCTACTTGGAAAC	960
DB	901	ACAGGTAACTTACCTTCCAGTCGGGAACCTAAATAATATCGTGCACCTACTTGGAAAC	960
QY	961	CTTATCCGTAAGCAACCAAGGGGATTTGCTCGGCACCTTGTCTCCCAAAAGTGTGACACA	1020
DB	961	CTTATCCGTAAGCAACCAAGGGGATTTGCTCGGCACCTTGTCTCCCAAAAGTGTGACACA	1020
QY	1021	GGTCGGTCTGTGATAGAGAACTTGCACACCTCATACTATAGAACTGACTTAGATTT	1080
DB	1021	GGTCGGTCTGTGATAGAGAACTTGCACACCTCATACTATAGAACTGACTTAGATTT	1080
QY	1081	ATATTGTACAAGAAATAGTAACTGTTCCCTATGTCCTCGGTATTTATTCCTGCTTGAGCGG	1140
DB	1081	ATATTGTACAAGAAATAGTAACTGTTCCCTATGTCCTCGGTATTTATTCCTGCTTGAGCGG	1140
QY	1141	CAATCGTGGGCTGTATGTACTCAAAGACCGAAGCGGCACTTACTACACCATACATGAC	1200
DB	1141	CAATCGTGGGCTGTATGTACTCAAAGACCGAAGCGGCACTTACTACACCATACATGAC	1200
QY	1201	TATCAAGGTTGAGTCAATCGCCAACTGCAAGATGACAAATGTAGATGTGTAACCCCCC	1260
DB	1201	TATCAAGGTTGAGTCAATCGCCAACTGCAAGATGACAAATGTAGATGTGTAACCCCCC	1260
QY	1261	GGGTATCATATCGCAAAACTATGGAGAAGCCGTGCTCTTAATAGATAAAACAATCATGCAA	1320
DB	1261	GGGTATCATATCGCAAAACTATGGAGAAGCCGTGCTCTTAATAGATAAAACAATCATGCAA	1320
QY	1321	TGTTTATCTTTAGGGGGGATTAATTTAAGGCTCAGTGGGGAATTCGATGTAACTTATCA	1380
DB	1321	TGTTTATCTTTAGGGGGGATTAATTTAAGGCTCAGTGGGGAATTCGATGTAACTTATCA	1380
QY	1381	GAAGATATCTCAATACAAAGTTCTCAAGTAATAATAACAGGCAATCTTGATATCTCAAC	1440
DB	1381	GAAGATATCTCAATACAAAGTTCTCAAGTAATAATAACAGGCAATCTTGATATCTCAAC	1440
QY	1441	TGAGCTTGGGAATGTCAACCAACTCGATCAGTAATGCTTTGAATAAGTTAGAGGAAACGAA	1500
DB	1441	TGAGCTTGGGAATGTCAACCAACTCGATCAGTAATGCTTTGAATAAGTTAGAGGAAACGAA	1500
QY	1501	CAGAAACTAGACAAAGTCAATGTCAAACTGACATAGCAATCTGTCTCATTAACCTATAT	1560
DB	1501	CAGAAACTAGACAAAGTCAATGTCAAACTGACATAGCAATCTGTCTCATTAACCTATAT	1560
QY	1561	CGTTTGTGACTATCATATCTCTTGTGTTTGGTATCTTACCTGATTTCTAGCATGCTACCT	1620
DB	1561	CGTTTGTGACTATCATATCTCTTGTGTTTGGTATCTTACCTGATTTCTAGCATGCTACCT	1620
QY	1621	AATGTACAAAGCAAAAGGCGCAACAAACCTTTATTTATGGCTTGGGAATAATACTCTAGA	1680
DB	1621	AATGTACAAAGCAAAAGGCGCAACAAACCTTTATTTATGGCTTGGGAATAATACTCTAGA	1680
QY	1681	TCAGATGAGAGCCACTACAAAAATGTGAACACAGATGAGGAAACGAAAGTTTCCCTAATAG	1740
DB	1681	TCAGATGAGAGCCACTACAAAAATGTGAACACAGATGAGGAAACGAAAGTTTCCCTAATAG	1740
QY	1741	TAAATTTGTGTAAGGTTCTGTTGTTTGGTATCTGTGAGTTAGAGGAAACCTACCGGT	1800
DB	1741	TAAATTTGTGTAAGGTTCTGTTGTTTGGTATCTGTGAGTTAGAGGAAACCTACCGGT	1800
QY	1801	TGTAGATGACCAAGGACGATATACGGGTAGAACCGTAAAGAGAGGCGCCCTCAATTCG	1860
DB	1801	TGTAGATGACCAAGGACGATATACGGGTAGAACCGTAAAGAGAGGCGCCCTCAATTCG	1860
QY	1861	GAGCCAGGCTTCAACCTCCGTTCTACCGCTTACCGGCAACAGTCTCAATCATGAGAC	1920
DB	1861	GAGCCAGGCTTCAACCTCCGTTCTACCGCTTACCGGCAACAGTCTCAATCATGAGAC	1920
QY	1921	CGCGCGTTAGCCAGTTGCGTTAGAGAAATGATGAAGAGAGGCAAAATACATGCGCG	1980
DB	1921	CGCGCGTTAGCCAGTTGCGTTAGAGAAATGATGAAGAGAGGCAAAATACATGCGCG	1980

QY 1981 TTGATATCCGGATTGCAATCTTATTCTTAACAGTAGTGACCTTGGCTATATCTGTAGCC 2040
Db 1981 TTGATATCCGGATTGCAATCTTATTCTTAACAGTAGTGACCTTGGCTATATCTGTAGCC 2040
QY 2041 TCCCTTTTATATAGCATGGGGCTAGCACACCTAGCGATCTTTAGGCATACCGACTAGG 2100
Db 2041 TCCCTTTTATATAGCATGGGGCTAGCACACCTAGCGATCTTTAGGCATACCGACTAGG 2100
QY 2101 ATTTCAGGGCAGAAAGAAAGATTACATCTACATCTGTTGTTCCAAATCAAGATGTAGAT 2160
Db 2101 ATTTCAGGGCAGAAAGAAAGATTACATCTACATCTGTTGTTCCAAATCAAGATGTAGAT 2160
QY 2161 AGGATATATAGCAAGTGGCCTTGGCTCGTTCGTTGGCAATGTTAAATCTGAGACCA 2220
Db 2161 AGGATATATAGCAAGTGGCCTTGGCTCGTTCGTTGGCAATGTTAAATCTGAGACCA 2220
QY 2221 ATTATGAACGCAATAAATCTCTCTCTTATCAGATTAAATGAGCTGCAAAACAAAGTGGG 2280
Db 2221 ATTATGAACGCAATAAATCTCTCTCTTATCAGATTAAATGAGCTGCAAAACAAAGTGGG 2280
QY 2281 TGGGGGGCACCTATCCATGACCCAGATTATATAGGGGGATAGGCAAGAACTCATTTGTA 2340
Db 2281 TGGGGGGCACCTATCCATGACCCAGATTATATAGGGGGATAGGCAAGAACTCATTTGTA 2340
QY 2341 GATGATGCTAGTGATGTACATCATCTTATCCCTCTGCAATTTCAAGAACATCTGAATTT 2400
Db 2341 GATGATGCTAGTGATGTACATCATCTTATCCCTCTGCAATTTCAAGAACATCTGAATTT 2400
QY 2401 ATCCGGGGCCTACTACAGGATCAGTTGCTCGACTCGAATACCTCATTTGACATCAGTGCT 2460
Db 2401 ATCCGGGGCCTACTACAGGATCAGTTGCTCGACTCGAATACCTCATTTGACATCAGTGCT 2460
QY 2461 ACCCATTACTGCTACACCCATAATGTATATTTGCTGGATGCAGAGATCACTCACATTC 2520
Db 2461 ACCCATTACTGCTACACCCATAATGTATATTTGCTGGATGCAGAGATCACTCACATTC 2520
QY 2521 TATCAGTATTAGACATTGGTGTCTCGGACATCTGCAACAGGAGGGTATCTTTTCT 2580
Db 2521 TATCAGTATTAGACATTGGTGTCTCGGACATCTGCAACAGGAGGGTATCTTTTCT 2580
QY 2581 ACTCTGGTTCATCAACTCGAGACACCCAAATCGGAAGTCTTCAGTGTGAGTGCA 2640
Db 2581 ACTCTGGTTCATCAACTCGAGACACCCAAATCGGAAGTCTTCAGTGTGAGTGCA 2640
QY 2641 ACTCCCTGGTGTGTGATATCTGTCTCGAAGTCAAGGACAGAGAGAAAGATTAT 2700
Db 2641 ACTCCCTGGTGTGTGATATCTGTCTCGAAGTCAAGGACAGAGAGAAAGATTAT 2700
QY 2701 AACTCAGTGTCCCTACCGGATGGTACATGGGAGTTAGGGTTGACGGCCAGTACAC 2760
Db 2701 AACTCAGTGTCCCTACCGGATGGTACATGGGAGTTAGGGTTGACGGCCAGTACAC 2760
QY 2761 GAAAGGACCTAGATGTACAACTATTTCGGGACCTGGGTGGCCAACTACCCAGGAGTA 2820
Db 2761 GAAAGGACCTAGATGTACAACTATTTCGGGACCTGGGTGGCCAACTACCCAGGAGTA 2820
QY 2821 GGGGGTGGATCTTTTATTGACAGCGCGTATGGTTCTCAGTCTACGGAGGTTAAAAACC 2880
Db 2821 GGGGGTGGATCTTTTATTGACAGCGCGTATGGTTCTCAGTCTACGGAGGTTAAAAACC 2880
QY 2881 AATTCAACCCAGTGCATGTACAGAAAGGAAATATGTATATCAAGCGATACAATGAC 2940
Db 2881 AATTCAACCCAGTGCATGTACAGAAAGGAAATATGTATATCAAGCGATACAATGAC 2940
QY 2941 ACATGCCAGATGACAGACTACAGATTCGAATGGCCAGTCTTCGTATAGCCCTGGA 3000
Db 2941 ACATGCCAGATGACAGACTACAGATTCGAATGGCCAGTCTTCGTATAGCCCTGGA 3000
QY 3001 CGGTTTGGTGGAAACGCATACAGCAGGCTATCTTATCTATCAAGGTGTCAACATCCTTA 3060
Db 3001 CGGTTTGGTGGAAACGCATACAGCAGGCTATCTTATCTATCAAGGTGTCAACATCCTTA 3060
QY 3061 GGGGAGACCCGGTACTGACTGTATCCGCCCAACACAGTCACTCATGGGGGGCGAAGGC 3120

Db 3061 GGGGAGACCCGGTACTGACTGTATCCGCCCAACACAGTCACTCATGGGGGGCGAAGGC 3120
QY 3121 AGAATTCTCAGTAGGACATCTCATTTCTTGTATCAACGAGGTCATCATACTTCTCT 3180
Db 3121 AGAATTCTCAGTAGGACATCTCATTTCTTGTATCAACGAGGTCATCATACTTCTCT 3180
QY 3181 CCGCGTTATATATCTTATGACAGTCAAGCAAAACAGCCACTCTTTCATAGTCTTAT 3240
Db 3181 CCGCGTTATATATCTTATGACAGTCAAGCAAAACAGCCACTCTTTCATAGTCTTAT 3240
QY 3241 ACATTCAATCGCTTCACTCGGCCAGGTAGTATCCCTTGCAGGCTTCAGCAAGATGCC 3300
Db 3241 ACATTCAATCGCTTCACTCGGCCAGGTAGTATCCCTTGCAGGCTTCAGCAAGATGCC 3300
QY 3301 AACTCGTGTGTACTGGAGTCTATACAGATCCATATCCCTTAATCTTCTATAGAAACC 3358
Db 3301 AACTCGTGTGTACTGGAGTCTATACAGATCCATATCCCTTAATCTTCTATAGAAACC 3358
RESULT 2
AAZ44617
ID AAZ44617 standard; DNA; 15186 BP.
XX
AC AAZ44617;
XX
DT 07-APR-2000 (first entry)
XX
DE Newcastle disease virus LaSota genomic DNA.
XX
KW Avian-paramyxovirus; infection; lentogenic; F protein; vaccine;
KW respiratory disease; gastrointestinal disease; poultry pathogen;
KW local immunity; ds.
XX
OS Newcastle disease virus.
XX
PH Key Location/Qualifiers
FT CDS 122..1591
FT FT /*tag= a
FT CDS 1887..3074
FT FT /*tag= b
FT CDS 3230..4384
FT FT /*tag= c
FT CDS 4544..6205
FT FT /*tag= d
FT CDS 6412..8145
FT FT /*tag= e
FT CDS 8381..14995
FT FT /*tag= f
XX
PN WO9966045-A1.
XX
PD 23-DEC-1999.
XX
PF 17-JUN-1999; 99WO-NL000377.
XX
PR 19-JUN-1998; 98EP-00202054.
XX
PA (DIEN-) STICHTING DIENST LANDBOUWKUNDIG ONDERZOE.
XX
PI Peeters BPH, De Leeuw OS, Koch G, Gielkens ALJ;
XX
DR WPI; 2000-106102/09.
XX
PT New avian paramyxovirus cDNA, useful for production of vaccine against
PT Newcastle disease virus.
XX
PS Disclosure; Fig 3; 115pp; English.
XX
CC This invention describes a novel avian-paramyxovirus cDNA (I) which
CC comprises a nucleic acid sequence corresponding to the 5' terminal end of
CC the genome of avian-paramyxovirus allowing the generation of an
CC infectious copy of avian-paramyxovirus. The cell line is useful for the

CC production of infectious lentogenic NDV (Newcastle Disease virus) without
CC the addition of exogenous proteolytic activity. Also it is possible to
CC generate a stable transfectant cell line that expresses the wild-type F
CC protein in the virus envelope therefore providing infectious particles,
CC useful in the form of a vaccine, especially against respiratory and/or
CC gastrointestinal diseases. NDV can be easily cultured to very high titers
CC in embryonated eggs. Mass culture of embryonated eggs is relatively
CC cheap. NDV vaccines are relatively stable and can be simply administered
CC by mass application methods e.g. drinking water or by spraying or by
CC aerosol formation. The natural route of infection is by the respiratory
CC and/or gastrointestinal tract which are also the major routes of
CC infection of many other poultry pathogens. NDV can induce local immunity
CC despite the presence of circulating maternal antibody. This sequence
CC represents the NDV strain LaSota genome DNA
XX
SQ

Sequence 15186 BP; 4431 A; 3544 C; 3462 G; 3749 T; 0 U; 0 Other;

Query Match 99.9%; Score 3353.2; DB 3; Length 15186;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3355; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	1	ACGGGTAGAAGATTCTCGATCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACC	60
DB	4498	ACGGGTAGAAGATTCTGGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACC	4557
QY	61	TTCTTACCAAGAACCCAGCACTATGATGCTGACTATCCGGGTTGGCGTGGCACTGAGTTG	120
DB	4558	TTCTTACCAAGAACCCAGCACTATGATGCTGACTATCCGGGTTGGCGTGGCACTGAGTTG	4617
QY	121	CATCTGTCCGGGAAAATCCCATTTGATGGCAGGCTCTTTCAGCTGCGAGGAATTTGGTTAC	180
DB	4618	CATCTGTCCGGGAAAATCCCATTTGATGGCAGGCTCTTTCAGCTGCGAGGAATTTGGTTAC	4677
QY	181	AGGAGCAAAAGCGTCAACATATACCTCATCCAGACAGGATCAATCATAGTTAAGCT	240
DB	4678	AGGAGCAAAAGCGTCAACATATACCTCATCCAGACAGGATCAATCATAGTTAAGCT	4737
QY	241	CCTCCCGAATCTGCCAAGGATAAGAGGCGATGCGGAAAGCCCTTGGATGCATACAA	300
DB	4738	CCTCCCGAATCTGCCAAGGATAAGAGGCGATGCGGAAAGCCCTTGGATGCATACAA	4797
QY	301	CAGGACATTCGCACTTTGCTACCCCTTTGGTGAATCTATCCGTAGGATACAAGATC	360
DB	4798	CAGGACATTCGCACTTTGCTACCCCTTTGGTGAATCTATCCGTAGGATACAAGATC	4857
QY	361	TGTGACTACATCTGGAGGGGGAGACAGGGCGCCCTTATAGGCGCCATTTATGGCGGTG	420
DB	4858	TGTGACTACATCTGGAGGGGGAGACAGGGCGCCCTTATAGGCGCCATTTATGGCGGTG	4917
QY	421	GGCTCTTTGGGTTGCAACTGCCGCACAAATAAAGAGCGCGCAGCTCTGATACAAGCCAA	480
DB	4918	GGCTCTTTGGGTTGCAACTGCCGCACAAATAAAGAGCGCGCAGCTCTGATACAAGCCAA	4977
QY	481	ACAAATGCTGCCAAATCTCCGACTTAAAGAGAGCATTTGCCGCAACCAATGAGGCTGT	540
DB	4978	ACAAATGCTGCCAAATCTCCGACTTAAAGAGAGCATTTGCCGCAACCAATGAGGCTGT	5037
QY	541	GCATGAGTCACTGACGGATTATCGCAACTAGCAGTGGCAGTTGGGAGAGTGCAGAGTT	600
DB	5038	GCATGAGTCACTGACGGATTATCGCAACTAGCAGTGGCAGTTGGGAGAGTGCAGAGTT	5097
QY	601	TGTTAATGACCAATTTAATAAAGAGCTCAGGAATTTAGACTGCATCAAAATTTGCAAGCA	660
DB	5098	TGTTAATGACCAATTTAATAAAGAGCTCAGGAATTTAGACTGCATCAAAATTTGCAAGCA	5157
QY	661	AGTTGGTGTAGACTCAACTGTACCTTAACCGAATTTAGCTACAGTATTCGGACCAAAAT	720
DB	5158	AGTTGGTGTAGACTCAACTGTACCTTAACCGAATTTAGCTACAGTATTCGGACCAAAAT	5217
QY	721	CACCTTCACCTGCTTAAACAGCTGACTATTTACGGACCTTTACAATCTAGCTGGTGGAA	780
DB	5218	CACCTTCACCTGCTTAAACAGCTGACTATTTACGGACCTTTACAATCTAGCTGGTGGAA	5277

QY	781	TATGGATTACTTATTACTAAGTTAGGTGTAGGGAAACAATCAACTCAGCTCATTAATCGG	840
DB	5278	TATGGATTACTTATTACTAAGTTAGGTGTAGGGAAACAATCAACTCAGCTCATTAATCGG	5337
QY	841	TAGCGGCTTAATCACCAGTAACCCCTATTCTATAGACTCACAGACTCAACTCTTGGGTAT	900
DB	5338	TAGCGGCTTAATCACCAGTAACCCCTATTCTATAGACTCACAGACTCAACTCTTGGGTAT	5397
QY	901	ACAGGTTAACTCTACCTTCAGTGGGAAACCTTAATAATATATGCGTGCCACCTTACCTTGA	960
DB	5398	ACAGGTTAACTCTACCTTCAGTGGGAAACCTTAATAATATATGCGTGCCACCTTACCTTGA	5457
QY	961	CTTATCCGTAAGCACACACAGGGGATTTGCCCTGGCACTTGTCCCAAAAGTGGTGACACA	1020
DB	5458	CTTATCCGTAAGCACACACAGGGGATTTGCCCTGGCACTTGTCCCAAAAGTGGTGACACA	5517
QY	1021	GGTGGGTTCTGTGATAGAGAACTTGACACCTCATACTGTATAGAACTTGACTTAGATT	1080
DB	5518	GGTGGGTTCTGTGATAGAGAACTTGACACCTCATACTGTATAGAACTTGACTTAGATT	5577
QY	1081	ATATTTGTCACAGAAATAGTAACGTTCCCTATGTCCCTGGTATTATTCTCTGCTTGA	1140
DB	5578	ATATTTGTCACAGAAATAGTAACGTTCCCTATGTCCCTGGTATTATTCTCTGCTTGA	5637
QY	1141	CAATACGTCCGGCTGTATGTACTCAAAGACCGAAGCGCACTTATACACCATACATGAC	1200
DB	5638	CAATACGTCCGGCTGTATGTACTCAAAGACCGAAGCGCACTTATACACCATACATGAC	5697
QY	1201	TATCAAAGGTTTCAGTGCATCGCCAACTGCAAGATGACAAACATGTAGATGTGTAAACCC	1260
DB	5698	TATCAAAGGTTTCAGTGCATCGCCAACTGCAAGATGACAAACATGTAGATGTGTAAACCC	5757
QY	1261	GGGTATCATATCGCAAAACCTATGCGAAGCGCTGTCTTAATAGATAAAACAATCATG	1320
DB	5758	GGGTATCATATCGCAAAACCTATGCGAAGCGCTGTCTTAATAGATAAAACAATCATG	5817
QY	1321	TGTTTTATCTTTAGCGGGGATAAATTTAAAGGCTCAGTGGGGAATTCGATGTAACTTAT	1380
DB	5818	TGTTTTATCTTTAGCGGGGATAAATTTAAAGGCTCAGTGGGGAATTCGATGTAACTTAT	5877
QY	1381	GAAGATATCTCAATACAAGATTTCTCAAGTAATAATAACAGGCAATCTTGATATCTCA	1440
DB	5878	GAAGATATCTCAATACAAGATTTCTCAAGTAATAATAACAGGCAATCTTGATATCTCA	5937
QY	1441	TGAGCTTTGGGAATGTCAACAACCTCGATCAGTAAATGCTTTGAATAAGTTAGAGGAA	1500
DB	5938	TGAGCTTTGGGAATGTCAACAACCTCGATCAGTAAATGCTTTGAATAAGTTAGAGGAA	5997
QY	1501	CAGAAAACCTAGACAAAGTCAATGTCAAACCTGACTAGCAATCTGTCTCTCATTAACCT	1560
DB	5998	CAGAAAACCTAGACAAAGTCAATGTCAAACCTGACTAGCAATCTGTCTCTCATTAACCT	6057
QY	1561	CGTTTTGACTATCATATCTCTTGTGTTTGGTATACCTTAGCCCTGATTTCTAGCATGCT	1620
DB	6058	CGTTTTGACTATCATATCTCTTGTGTTTGGTATACCTTAGCCCTGATTTCTAGCATGCT	6117
QY	1621	AATGTACAAGCAAAAGCGCAACAAAAACCTTTATTTATGCTTGGGAAATAACTCTAGA	1680
DB	6118	AATGTACAAGCAAAAGCGCAACAAAAACCTTTATTTATGCTTGGGAAATAACTCTAGA	6177
QY	1681	TCAGATGAGAGCCACTACAAAAATGTGAACACAGATGAGGAAACGAAGTTTCCCTAAT	1740
DB	6178	TCAGATGAGAGCCACTACAAAAATGTGAACACAGATGAGGAAACGAAGTTTCCCTAAT	6237
QY	1741	TAAATTTGTGAAAGTTCTGTGATGCTGTCTGATTTAGAGAGTTAGAAAAAATACCCGT	1800
DB	6238	TAAATTTGTGAAAGTTCTGTGATGCTGTCTGATTTAGAGAGTTAGAAAAAATACCCGT	6297
QY	1801	TGTAGATGACCAAGAGCCATATACGGGTAGAACCGTAAAGAGAGGCGCCCTCAATTC	1860
DB	6298	TGTAGATGACCAAGAGCCATATACGGGTAGAACCGTAAAGAGAGGCGCCCTCAATTC	6357
QY	1861	GAGCCAGGCTTCACAAACCTCCGTTCTACCGCTTTCACCGCAACACAGTCTCAATCAT	1920

Db 6358 GAGCCAGGCTTACAACTCCGTTCTACCGCTTCCGCAACAGTCTCAATCATGGAC 6417
Qy 1921 CGCGCGTTAGCCCAAGTTGCGTTAGAGAAATGATGAAGAGAGGCAAAAATACATGGCG 1980
Db 6418 CGCGCGTTAGCCCAAGTTGCGTTAGAGAAATGATGAAGAGAGGCAAAAATACATGGCG 6477
Qy 1981 TTGATATCCGGATTGCAATCTTATCTTAACAGTAGTGACCTGGCTGTATATCTGTAGCC 2040
Db 6478 TTGATATCCGGATTGCAATCTTATCTTAACAGTAGTGACCTGGCTGTATATCTGTAGCC 6537
Qy 2041 TCCCTTTTATATAGCAGGGGCTAGCACACTAGCGATCTTGTAGGCATACCGACTAGG 2100
Db 6538 TCCCTTTTATATAGCAGGGGCTAGCACACTAGCGATCTTGTAGGCATACCGACTAGG 6597
Qy 2101 ATTTCCAGGGCAGAGAAAGATTACATCTACACTTGGTTCCTCAATCAAGATTGTAGTAGAT 2160
Db 6598 ATTTCCAGGGCAGAGAAAGATTACATCTACACTTGGTTCCTCAATCAAGATTGTAGTAGAT 6657
Qy 2161 AGGATATATAGCAAGTGGCCCTTGAGTCTCGTGGTGGCAATGTTAAATACATGAGACACCA 2220
Db 6658 AGGATATATAGCAAGTGGCCCTTGAGTCTCGTGGTGGCAATGTTAAATACATGAGACACCA 6717
Qy 2221 ATTATGAACGCAATAACATCTCTCTCTATCAGATTAAATGAGCTGCAAAACACAGTGGG 2280
Db 6718 ATTATGAACGCAATAACATCTCTCTCTATCAGATTAAATGAGCTGCAAAACACAGTGGG 6777
Qy 2281 TCGGGGGCACCTATCCATGACCCAGATTATATAGGGGGGATAGGCAAAAGAACTCATTTGTA 2340
Db 6778 TCGGGGGCACCTATCCATGACCCAGATTATATAGGGGGGATAGGCAAAAGAACTCATTTGTA 6837
Qy 2341 GATGATGTAGTAGTGTCACATCAATCTATCCCTCTGCAATTCATCAAGAACATCTGAATTTT 2400
Db 6838 GATGATGTAGTAGTGTCACATCAATCTATCCCTCTGCAATTCATCAAGAACATCTGAATTTT 6897
Qy 2401 ATCCCGGCGCTACTACAGGATCAGGTGGCACTCGAATACCTCATTTTGACATGAGTCT 2460
Db 6998 ATCCCGGCGCTACTACAGGATCAGGTGGCACTCGAATACCTCATTTTGACATGAGTCT 6957
Qy 2461 ACCCATTAATGCTACACCCCAATGTAATATGTTGCTGATGAGAGATCACTCACATTC 2520
Db 6958 ACCCATTAATGCTACACCCCAATGTAATATGTTGCTGATGAGAGATCACTCACATTC 7017
Qy 2521 TATCAGTATTTAGCACTTTGGTGTCTCCGACATCTGCAACAGGAGGGTATCTTTCT 2580
Db 7018 TATCAGTATTTAGCACTTTGGTGTCTCCGACATCTGCAACAGGAGGGTATCTTTCT 7077
Qy 2581 ACTCTGCGTTCCATCAACTGACGACACACCCAAATCGGAATCGAATACCTCATTTTGACATGAGTCT 2640
Db 7078 ACTCTGCGTTCCATCAACTGACGACACACCCAAATCGGAATCGAATACCTCATTTTGACATGAGTCT 7137
Qy 2641 ACTCCCTGGGTTGTGATATGCTGTCTCGAAAGTCACGGAGACAGAGGAAGAAAGATTAT 2700
Db 7138 ACTCCCTGGGTTGTGATATGCTGTCTCGAAAGTCACGGAGACAGAGGAAGAAAGATTAT 7197
Qy 2701 AACTCAGCTGTCCCTACCGGATGATACATGGGAGTTAGGGTTTCGACGGCCAGTACCAC 2760
Db 7198 AACTCAGCTGTCCCTACCGGATGATACATGGGAGTTAGGGTTTCGACGGCCAGTACCAC 7257
Qy 2761 GAAAAGGACCTAGATGTCAACATTAATTCGGGACCTGGGTGGCCAACTACCCAGGAGTA 2820
Db 7258 GAAAAGGACCTAGATGTCAACATTAATTCGGGACCTGGGTGGCCAACTACCCAGGAGTA 7317
Qy 2821 GGGGTGATCTTTTATTGACAGCCGCTATGTTCTCAGCTCAGGAGGTTAAACCC 2880
Db 7318 GGGGTGATCTTTTATTGACAGCCGCTATGTTCTCAGCTCAGGAGGTTAAACCC 7377
Qy 2881 AATTCCAGCTGACACTGTACAGAGGGGAAATATGTATATACAGCGATACAAATGAC 2940
Db 7378 AATTCCAGCTGACACTGTACAGAGGGGAAATATGTATATACAGCGATACAAATGAC 7437
Qy 2941 ACATGCCAGATAGCAAGATACAGATTCGATGGCCAAAGTCTTGTATTAAGCCTGGA 3000

Db 7438 ACATGCCAGATGAGCAAGACTACCAGATTCGATGGCCAGTCTTGTATTAAGCCTGGA 7497
Qy 3001 CGGTTTGGTGGGAAACCCATACAGCAGCGGTATCTTATCTATCAAGGTGTCAACATCTTA 3060
Db 7498 CGGTTTGGTGGGAAACCCATACAGCAGCGGTATCTTATCTATCAAGGTGTCAACATCTTA 7557
Qy 3061 GGCGAAGACCCGGTACTGACTGTACCGCCCAACACAGTCACTCATGGGGCCGAAGGC 3120
Db 7558 GGCGAAGACCCGGTACTGACTGTACCGCCCAACACAGTCACTCATGGGGCCGAAGGC 7617
Qy 3121 AGAATTCATCAGTAGGAGCATCTCTTCTTGTATCAACGAGGGTCACTATCTTCTCT 3180
Db 7618 AGAATTCATCAGTAGGAGCATCTCTTCTTGTATCAACGAGGGTCACTATCTTCTCT 7677
Qy 3181 CCOCGGTTATATATCTATGACAGTCAAGCAAAACAGCACTCTTATAGTCTTAT 3240
Db 7678 CCOCGGTTATATATCTATGACAGTCAAGCAAAACAGCACTCTTATAGTCTTAT 7737
Qy 3241 ACATTCAATGCCCTCACTCGGCCAGGTAGTATCCCTTGCAGGCTTCAGCAAGATGCCCC 3300
Db 7738 ACATTCAATGCCCTCACTCGGCCAGGTAGTATCCCTTGCAGGCTTCAGCAAGATGCCCC 7797
Qy 3301 AACTCGTGTACTGAGTCTATACAGATCCATATCCCTATCTTCTATAGAAACC 3358
Db 7798 AACTCGTGTACTGAGTCTATACAGATCCATATCCCTATCTTCTATAGAAACC 7855

RESULT 3
ADH71088
ID ADH71088 standard; DNA; 15186 BP.
XX
AC ADH71088;
XX
DT 25-MAR-2004 (first entry)
XX
DE Newcastle disease virus HN gene.
XX
KW Virucide; vaccine accelerator factor; VAF; immuno-stimulant;
KW viral vaccine; Marek's disease virus; MDV;
KW infectious bursal disease virus; IBDV; Newcastle disease virus; NDV;
KW infectious bronchitis virus; IBV; fowlpox virus; FPV;
KW infectious laryngotracheitis virus; ILTV; avian encephalomyelitis virus;
KW AEV; avian leukosis virus; ALV; avian parainfluenza virus; APV;
KW duck hepatitis virus; DHV; hemorrhagic enteritis virus; HEV; HN; ds.
XX
OS Newcastle disease virus.
XX
PN US2003207836-A1.
XX
PD 06-NOV-2003.
XX
PF 06-MAY-2003; 2003US-00429735.
XX
PR 08-MAR-2002; 2002US-0362547P.
PR 04-MAR-2003; 2003US-00377718.
XX
PA (KUOT/) KUO T Y.
XX
PI Kuo TY;
XX
DR WPI; 2003-875897/81.
XX
PT New vaccine accelerator factor (VAF) comprising one or more DNA
PT constructs, each comprising a DNA molecule and a vector, useful as a
PT vaccine for viruses that affect chicken.
XX
PS Claim 13; SEQ ID NO 3; 28pp; English.
XX
CC The present invention provides a vaccine accelerator factor (VAF) which
CC is an in ovo nucleotide immuno-stimulant. The VAF comprises one or more
CC DNA constructs, each comprising a DNA molecule and a vector, where each
CC of the DNA molecule contains one or more genes or gene fragments each
CC encoding an antigenic peptide of an avian virus. VAF accelerates and

CC stimulates a protective immune response of a viral vaccine against the
CC avian virus. VAF is useful as a vaccine against Marek's disease virus
CC (MDV), infectious bursal disease virus (IBDV), Newcastle disease virus
CC (NDV), infectious bronchitis virus (IBV), fowlpox virus (FPV), infectious
CC laryngotracheitis virus (ILT), avian encephalomyelitis virus (AEV),
CC avian leukosis virus (ALV), avian parainfluenza virus (APV), duck
CC hepatitis virus (DHV) and hemorrhagic enteritis virus (HEV) in chicken.
CC The present sequence is NDV HN gene.
XX
SQ Sequence 15186 BP; 4431 A; 3542 C; 3464 G; 3749 T; 0 U; 0 Other;
Query Match 99.9%; Score 3353.2; DB 10; Length 15186;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3355; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ACGGGTAGAGATTCTCGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGCTCCAGACC 60
DB 4498 ACGGGTAGAGATTCTCGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGCTCCAGACC 4557
QY 61 TTCTACCAAGAACCCAGCACCTATGATGCTGACTATATCCGGGTTGCGCTGGCACTGAGTTG 120
DB 4558 TTCTACCAAGAACCCAGCACCTATGATGCTGACTATATCCGGGTTGCGCTGGCACTGAGTTG 4617
QY 121 CATCTGTCGGGCAAACTCCATTGATGGGAGGCTCTTGGAGCTGCGAGGAATTGTTGTTAC 180
DB 4618 CATCTGTCGGGCAAACTCCATTGATGGGAGGCTCTTGGAGCTGCGAGGAATTGTTGTTAC 4677
QY 181 AGGAGACAAGCCGTCAACATATACCTCATCCAGCAGGATCAATCATAGTTAAGCT 240
DB 4678 AGGAGACAAGCCGTCAACATATACCTCATCCAGCAGGATCAATCATAGTTAAGCT 4737
QY 241 CCTCCCGAATCTGCCAAGGATAGGAGGATGTCGAAAGCCCTTGGATGCATACAA 300
DB 4738 CCTCCCGAATCTGCCAAGGATAGGAGGATGTCGAAAGCCCTTGGATGCATACAA 4797
QY 301 CAGACATATGACCATTTGCTCAACCCCTTGGTGTGACTATCCGTTAGGATACAAAGTTC 360
DB 4798 CAGACATATGACCATTTGCTCAACCCCTTGGTGTGACTATCCGTTAGGATACAAAGTTC 4857
QY 361 TGTGACTACATCTCGAGGGGGGACAGGGCGGCTTATAGGCGGCATTTATGGCGGTGT 420
DB 4858 TGTGACTACATCTCGAGGGGGGACAGGGCGGCTTATAGGCGGCATTTATGGCGGTGT 4917
QY 421 GGCTCTTGGGGTTGCAACTGCGGCAAAATAACAGCGCGCGAGCTCTGTATACAAAGCAA 480
DB 4918 GGCTCTTGGGGTTGCAACTGCGGCAAAATAACAGCGCGCGAGCTCTGTATACAAAGCAA 4977
QY 481 AAAAAATGCTGCCAAATCTCTCGACTTAAAGAGAGCAATTCGCGCAACCAATGAGGCTGT 540
DB 4978 AAAAAATGCTGCCAAATCTCTCGACTTAAAGAGAGCAATTCGCGCAACCAATGAGGCTGT 5037
QY 541 GCATGAGGTCACTGACGGATTATCGCACTAGCAGTGGCAGTTGGGAGATGGCAGGTT 600
DB 5038 GCATGAGGTCACTGACGGATTATCGCACTAGCAGTGGCAGTTGGGAGATGGCAGGTT 5097
QY 601 TGTAAATGACCAATTTAAATAAACAGCTCAGGAATTAGACTGCAATCAAAATTCGACAGCA 660
DB 5098 TGTAAATGACCAATTTAAATAAACAGCTCAGGAATTAGACTGCAATCAAAATTCGACAGCA 5157
QY 661 AGTTGGTGTAGAGCTCAACCTGTACCTAACCGAATTGACTACAGTATTCGGACCACAAT 720
DB 5158 AGTTGGTGTAGAGCTCAACCTGTACCTAACCGAATTGACTACAGTATTCGGACCACAAT 5217
QY 721 CACTTCACCTGCTTAAACAGCTGACTATTCAGGCACTTTACATCTAGCTGGTGAAA 780
DB 5218 CACTTCACCTGCTTAAACAGCTGACTATTCAGGCACTTTACATCTAGCTGGTGAAA 5277
QY 781 TATGGAATTAATTTAGTAAAGTTAGGTGTAGGGAACAATCAACTCAGCTCATTAATCGG 840
DB 5278 TATGGAATTAATTTAGTAAAGTTAGGTGTAGGGAACAATCAACTCAGCTCATTAATCGG 5337
QY 841 TAGCGGCTTAATCAACCGGTAAACCTATTTCTATACGACTCAAGACTCAATCTTGGGTAT 900
DB

DB 5338 TAGCGGCTTAATCAACCGGTAAACCTATTCTATACGACTCACAGACTCAACTCTTGGGTAT 5397
QY 901 ACAGGTAACTTACCTTTAGTCGGGAACCTAAATAATATGCGTGGCCACTTCTTGGAAAC 960
DB 5398 ACAGGTAACTTACCTTTAGTCGGGAACCTAAATAATATGCGTGGCCACTTCTTGGAAAC 5457
QY 961 CTTATCCGTAAGCAACACAGGGGATTTGCTGCGGCACTTGTCCCAAAAGTGGTGACACA 1020
DB 5458 CTTATCCGTAAGCAACACAGGGGATTTGCTGCGGCACTTGTCCCAAAAGTGGTGACACA 5517
QY 1021 GGTGCGGTTCTGTGATAGAGAACTTCACACACTCATACTGTATAGAACTGACTTACATTT 1080
DB 5518 GGTGCGGTTCTGTGATAGAGAACTTCACACACTCATACTGTATAGAACTGACTTACATTT 5577
QY 1081 ATATTCTCAAGAATAAGTAAACGTTCCCTATGTCCCTGGTATTATTCCTGCTTGAACGG 1140
DB 5578 ATATTCTCAAGAATAAGTAAACGTTCCCTATGTCCCTGGTATTATTCCTGCTTGAACGG 5637
QY 1141 CAATACGTCGGCTGTATGTATCTCAAGAACCAGAGCGCACTTATCTACACCATATGAC 1200
DB 5638 CAATACGTCGGCTGTATGTATCTCAAGAACCAGAGCGCACTTATCTACACCATATGAC 5697
QY 1201 TATCAAGGTTGAGTTCATCGCCCACTGCAAGATGACCAATGTAGATGTGTAACCCCCC 1260
DB 5698 TATCAAGGTTGAGTTCATCGCCCACTGCAAGATGACCAATGTAGATGTGTAACCCCCC 5757
QY 1261 GGGTATCATATCGCAAACTATGGAGAGCGGTCTCTAATAAGATAAAACAATCATGCAA 1320
DB 5758 GGGTATCATATCGCAAACTATGGAGAGCGGTCTCTAATAAGATAAAACAATCATGCAA 5817
QY 1321 TGTGTTTATCCTTAGGCGGATTAACCTTAAAGGCTCAGTGGGGAATTCGATGTAACTTATCA 1380
DB 5818 TGTGTTTATCCTTAGGCGGATTAACCTTAAAGGCTCAGTGGGGAATTCGATGTAACTTATCA 5877
QY 1381 GAAGATAATCTCAATACAGATTCTCAAGTATATAAAGAGGCAATCTTGATATCTCAAC 1440
DB 5878 GAAGATAATCTCAATACAGATTCTCAAGTATATAAAGAGGCAATCTTGATATCTCAAC 5937
QY 1441 TGAGCTTGGGAATGTCAACAACTCGATAGTAACTGCTTGAATAAGTTAGAGGAAAGCAA 1500
DB 5938 TGAGCTTGGGAATGTCAACAACTCGATAGTAACTGCTTGAATAAGTTAGAGGAAAGCAA 5997
QY 1501 CAGAAAATAGACAAAGTCAATGTCAAACTGACTAGCAATCTGCTCTCATTTACCTATAT 1560
DB 5998 CAGAAAATAGACAAAGTCAATGTCAAACTGACTAGCAATCTGCTCTCATTTACCTATAT 6057
QY 1561 CGTTTGTGATCTATCATATCTCTGTTTGGTATACCTAGCTGATTTAGCTAGCTACCT 1620
DB 6058 CGTTTGTGATCTATCATATCTCTGTTTGGTATACCTAGCTGATTTAGCTAGCTACCT 6117
QY 1621 AATGTACAAAGCAAGCGGCACAAACCAACCTTATTATGGCTTGGGAATAAATACTCTAGA 1680
DB 6118 AATGTACAAAGCAAGCGGCACAAACCAACCTTATTATGGCTTGGGAATAAATACTCTAGA 6177
QY 1681 TCAGATGAGAGCCACTACAAAAATGTGAACACAGATGAGGAACGAAGTTTCCCTAATAG 1740
DB 6178 TCAGATGAGAGCCACTACAAAAATGTGAACACAGATGAGGAACGAAGTTTCCCTAATAG 6237
QY 1741 TAAATTTGTGAAAAGTTCTGTTAGTCTGTGAGTTCAGTTCAGAGAGTTAAGAAAAAATACCGGT 1800
DB 6238 TAAATTTGTGAAAAGTTCTGTTAGTCTGTGAGTTCAGTTCAGAGAGTTAAGAAAAAATACCGGT 6297
QY 1801 TGTAGATGACCAAGGACGATATACGGGTAGAACCGTTAGAGAGGCGCGCCCTCAATTGC 1860
DB 6298 TGTAGATGACCAAGGACGATATACGGGTAGAACCGTTAGAGAGGCGCGCCCTCAATTGC 6357
QY 1861 GAGCCAGGCTTCAACCTCCGTTTACCGCTTACCGCAACACAGTCTCTCAATCATGGAC 1920
DB 6358 GAGCCAGGCTTCAACCTCCGTTTACCGCTTACCGCAACACAGTCTCTCAATCATGGAC 6417
QY 1921 CGCGCGCTTAGCCAAAGTTGCGTTAGAGATGATGAAGAGGCAAAAAATATACATGGCGC 1980
DB 6418 CGCGCGCTTAGCCAAAGTTGCGTTAGAGATGATGAAGAGGCAAAAAATATACATGGCGC 6477

Qy	1981	TTGATATTCCGGATTGCAATCTTATTCTTAAACAGTAGTGACCTTGGCTATATCTGTAGCC	2040
Db	6478	TTGATATTCCGGATTGCAATCTTATTCTTAAACAGTAGTGACCTTGGCTATATCTGTAGCC	6537
Qy	2041	TCCCTTTTATATAGCATGGGGCTAGACACCTTAGCGCATCTTGTAGGCATACCGACTAGG	2100
Db	6538	TCCCTTTTATATAGCATGGGGCTAGACACCTTAGCGCATCTTGTAGGCATACCGACTAGG	6597
Qy	2101	ATTTCCAGGCGAAGAAGAAATACATCTACACTTCGTTTCCAATCAAGATGTAGTAGAT	2160
Db	6598	ATTTCCAGGCGAAGAAGAAATACATCTACACTTCGTTTCCAATCAAGATGTAGTAGAT	6657
Qy	2161	AGGATATATAAGCAAGTGGCCCTTGAATCTCGTGTGGCATTTGTTAAATACTGAGACCA	2220
Db	6658	AGGATATATAAGCAAGTGGCCCTTGAATCTCGTGTGGCATTTGTTAAATACTGAGACCA	6717
Qy	2221	ATTATGAACCAATAACATCTCTCTTATCAGATTAATGGAGCTGCAAAACAACAGTGG	2280
Db	6718	ATTATGAACCAATAACATCTCTCTTATCAGATTAATGGAGCTGCAAAACAACAGTGG	6777
Qy	2281	TGGGGGCACTATCCATGACCCAGATTATATAGGGGGATAGGCAAGAACTCATTTGTA	2340
Db	6778	TGGGGGCACTATCCATGACCCAGATTATATAGGGGGATAGGCAAGAACTCATTTGTA	6837
Qy	2341	GATGATCTATGATGTCAACATATCTATCCCTCTGCAATTCAGAAACATCTGAATTTT	2400
Db	6838	GATGATCTATGATGTCAACATATCTATCCCTCTGCAATTCAGAAACATCTGAATTTT	6897
Qy	2401	ATCCCGCGCTACTACAGGATCAGTTGCATCCGAATACCCTCATTTGATGATGAGTCT	2460
Db	6898	ATCCCGCGCTACTACAGGATCAGTTGCATCCGAATACCCTCATTTGATGAGTCT	6957
Qy	2461	ACCCATTACTGTACACCCATAATGTATTTGTCTGGATGCGAGATCACTCACATTTCA	2520
Db	6958	ACCCATTACTGTACACCCATAATGTATTTGTCTGGATGCGAGATCACTCACATTTCA	7017
Qy	2521	TATCAGTATTTAGCACTTGGTGTCTCCGACATCTCGAACAAGGGAGGTATTTCTTCT	2580
Db	7018	TATCAGTATTTAGCACTTGGTGTCTCCGACATCTCGAACAAGGGAGGTATTTCTTCT	7077
Qy	2581	ACTCTGGTTCATCAACCTGGACGACACCCAAATCGGAAGTCTTCAGTGTGAGTGCA	2640
Db	7078	ACTCTGGTTCATCAACCTGGACGACACCCAAATCGGAAGTCTTCAGTGTGAGTGCA	7137
Qy	2641	ACTCCCCTGGTGTGTATGCTGTCTCGAAAGTCAACCGAGAGAGAGATTTAT	2700
Db	7138	ACTCCCCTGGTGTGTATGCTGTCTCGAAAGTCAACCGAGAGAGAGATTTAT	7197
Qy	2701	AATCTAGCTGTCCCTACCGGATGGTACATGGGAGGTTAGGGTTCGACGGCAGTACCAC	2760
Db	7198	AATCTAGCTGTCCCTACCGGATGGTACATGGGAGGTTAGGGTTCGACGGCAGTACCAC	7257
Qy	2761	GAAAGGACCTAGATGTCAACAATATTTCGGGACCTGGGTGGCCAACTACCCAGGAGTA	2820
Db	7258	GAAAGGACCTAGATGTCAACAATATTTCGGGACCTGGGTGGCCAACTACCCAGGAGTA	7317
Qy	2821	GGGGTGGATCTTTTATTTGACAGCCCGTATGGTCTCAGTCTACGAGGGTTAAAAACC	2880
Db	7318	GGGGTGGATCTTTTATTTGACAGCCCGTATGGTCTCAGTCTACGAGGGTTAAAAACC	7377
Qy	2881	AATTCAACCCAGTGACATGTACAGGAGGGGAATATGTGATATACAGCGATCAATGAC	2940
Db	7378	AATTCAACCCAGTGACATGTACAGGAGGGGAATATGTGATATACAGCGATCAATGAC	7437
Qy	2941	ACATGCCAGATGAGCAAGACTACAGATTCGAATGCGCAAGTCTTCTGTAATAGCCCTGGA	3000
Db	7438	ACATGCCAGATGAGCAAGACTACAGATTCGAATGCGCAAGTCTTCTGTAATAGCCCTGGA	7497
Qy	3001	CGGTTTGGTGGGAAACGCATACAGCAGGCTATTTATCTATCAAGGTGTCAACATCTTTA	3060
Db	7498	CGGTTTGGTGGGAAACGCATACAGCAGGCTATTTATCTATCAAGGTGTCAACATCTTTA	7557

QY	3061	GGCGAAGACCGGGTACTGACTGTATACCGCCCAACAACAGTCACTCATCTATGGGGGCGGAAGGC	3121
DB	7558	GGCGAAGACCGGGTACTGACTGTATACCGCCCAACAACAGTCACTCATCTATGGGGGCGGAAGGC	7617
QY	3121	AGAATTCTCACAGTAGGACAATCTCATTTCTTGTTATCAACGAGGGTCAATCATACTTCTCT	3180
DB	7618	AGAATTCTCACAGTAGGACAATCTCATTTCTTGTTATCAACGAGGGTCAATCATACTTCTCT	7677
QY	3181	CCCGCGTTATTTATATCTTATGACAGTCAGCAACAAAAACAGCCACTCTTTCATAGTCCCTTAT	3240
DB	7678	CCCGCGTTATTTATATCTTATGACAGTCAGCAACAAAAACAGCCACTCTTTCATAGTCCCTTAT	7737
QY	3241	ACATTTCAATGCCTTCACTCCGCCAGGTAGTATCCCTTCCAGGCTTCAGCAAGATGCCCC	3300
DB	7738	ACATTTCAATGCCTTCACTCCGCCAGGTAGTATCCCTTCCAGGCTTCAGCAAGATGCCCC	7797
QY	3301	AACTCGTGTGTTACTGAGAGTCTATACAGATCCCATATCCCCTAATCTTCTATAGAAGCC	3358
DB	7798	AACTCGTGTGTTACTGAGAGTCTATACAGATCCCATATCCCCTAATCTTCTATAGAAGCC	7855

RESULT 4
ADH62844
ID ADH62844 standard; DNA; 15186 BP

XX Multiple DNA vaccine for in ovo injection, useful for inducing protective
PT immune response against the avian viral diseases in fowl, comprises two
PT or more DNA constructs.
XX
XX Claim 10; SEQ ID NO 3; 26pp; English.
PS
XX The invention relates to multiple and multivalent DNA vaccine for in ovo
CC infection which comprises two or more DNA constructs, where each DNA
CC construct expresses an antigenic protein of an avian virus causing avian
CC viral disease in fowl. The antigenic protein of the avian virus is
CC capable of inducing a protective immune response against the avian viral
CC disease in the fowl. The vaccine is useful for inducing protective immune
CC response against the avian viral diseases in fowl. The present sequence
CC is Newcastle disease virus (NDV) haemagglutinin neuraminidase (HN) gene
CC used in multiple and multivalent DNA vaccine.
CC

Sequence 15186 BP: 4431 A; 3542 C; 3464 G; 3749 T; 0 U; 0 Other;

Query Match	99.9%	Score 3553.2	DB 10	Length 15186
Best Local Similarity	99.9%	Pred. No. 0		
Matches 3355	Conservative	0	Mismatches 3	Indels 0
				Gaps 0

Best Local Similarity 99.9%; Pred. NO. 0;
Matches 3355; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Query Match 99.9%; Score 3353.2; DB 10; Length 15186

Query Match 99.5%; Score 333.2
Best Local Similarity 99.9%; Pred. No. 0;

Matches 3355; Conservative	0; Mismatches	3; Indels	0; Gaps	0;
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Sequence 15186 BP: 4431 A; 3542 C; 3464 G; 3749 T; 0 U; 0 Other;

Query Match 99.9%; Score 3353.2; DB 10; Length 15186

Query Match 99.5%; Score 333.2
Best Local Similarity 99.9%; Pred. No. 0;

Matches 3355; Conservative	0; Mismatches	3; Indels	0; Gaps	0;
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Qy	1	ACGGGTAGAAGATTCTGTGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACC	60
Db	4498	ACGGGTAGAAGATTCTGTGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACC	4557
Qy	61	TTCTACCAAGAACCCAGCCTATGATGCTGACTATCGGGTTGGCTGGCACTGAGTTG	120
Db	4558	TTCTACCAAGAACCCAGCCTATGATGCTGACTATCGGGTTGGCTGGCACTGAGTTG	4617
Qy	121	CATCTGTCGGGCAAACTCCAATTGATGGCAGCGCTCTTGCAGCTGCAGGAATTGGGTTAC	180
Db	4618	CACTCTGTCGGGCAAACTCCAATTGATGGCAGCGCTCTTGCAGCTGCAGGAATTGGGTTAC	4677
Qy	181	AGGAGACAAAGCCGCTCAACATATACACCTCATCCAGACAGGATCAATCATAGTTAAGCT	240
Db	4678	AGGAGACAAAGCCGCTCAACATATACACCTCATCCAGACAGGATCAATCATAGTTAAGCT	4737
Qy	241	CCTCCCGAACTGCCCAAGGATAGGAGGCATGTGCGAAAGCCCCCTTGGATGCATACAA	300
Db	4738	CCTCCCGAACTGCCCAAGGATAGGAGGCATGTGCGAAAGCCCCCTTGGATGCATACAA	4797
Qy	301	CAGGACATTGACCACTTTGCTCACCCCTTTGGTGACTCTATCCGTAGGATACAAAGATC	360
Db	4798	CAGGACATTGACCACTTTGCTCACCCCTTTGGTGACTCTATCCGTAGGATACAAAGATC	4857
Qy	361	TGTGACTACATCTGGAGGGGGGAGACAGGGCGGCTTTATAGGCGCCATTTATGGCGGTG	420
Db	4858	TGTGACTACATCTGGAGGGGGGAGACAGGGCGGCTTTATAGGCGCCATTTATGGCGGTG	4917
Qy	421	GGCTCTTTGGGGTTGCAACTGCCGACAAATAACAGCGGCGCAGCTCTGATACAGCCAA	480
Db	4918	GGCTCTTTGGGGTTGCAACTGCCGACAAATAACAGCGGCGCAGCTCTGATACAGCCAA	4977
Qy	481	ACAAAATGCTGCCAAACATCTCCGACTTAAAGAGAGCATTTGCCGCAACCAATGAGGCTGT	540
Db	4978	ACAAAATGCTGCCAAACATCTCCGACTTAAAGAGAGCATTTGCCGCAACCAATGAGGCTGT	5037
Qy	541	GCA TAGGTCACCTGACCGGATTA TCGCAACTAGCAGTGGCGAGTTGGGAAGATGCA GCA GTT	600
Db	5038	GCA TAGGTCACCTGACCGGATTA TCGCAACTAGCAGTGGCGAGTTGGGAAGATGCA GCA GTT	5097
Qy	601	TGTTAATGACCAATTTAATAAACAGCTCAGGAATTAGACTGATCAAAATTCGACAGCA	660
Db	5098	TGTTAATGACCAATTTAATAAACAGCTCAGGAATTAGACTGATCAAAATTCGACAGCA	5157
Qy	661	AGTTGGTGTAGAGCTCAACTGTACCTAACCGAATTGACTACAGTATTCGGACCAAAAT	720
Db	5158	AGTTGGTGTAGAGCTCAACTGTACCTAACCGAATTGACTACAGTATTCGGACCAAAAT	5217
Qy	721	CACCTCACCTGCTTTAAACAAGCTGACTATTTCAGGCACTTTACAATCTAGCTGGTGGAAA	780
Db	5218	CACCTCACCTGCTTTAAACAAGCTGACTATTTCAGGCACTTTACAATCTAGCTGGTGGAAA	5277
Qy	781	TATGGATTACTTATGACTAAGTTAGTTAGTTAGGAAACAATCAACTCAGCTCATTAATCGG	840
Db	5278	TATGGATTACTTATGACTAAGTTAGTTAGTTAGGAAACAATCAACTCAGCTCATTAATCGG	5337
Qy	841	TAGCGGCTTAATCAACGGTAAACCTATCTTATACGACTACAGACTCAACTCTTTGGGTAT	900
Db	5338	TAGCGGCTTAATCAACGGTAAACCTATCTTATACGACTACAGACTCAACTCTTTGGGTAT	5397
Qy	901	ACAGGTAACCTACCTTCAGTCGGGAACTTAAATAATATATCGTGCCCACTTCTGGAAC	960
Db	5398	ACAGGTAACCTACCTTCAGTCGGGAACTTAAATAATATATCGTGCCCACTTCTGGAAC	5457
Qy	961	CTTATCCGTAAAGCAACACAGGGGATTTGGCTGGGCACTTGTCCCAAAAGTGGTGACAC	1020
Db	5458	CTTATCCGTAAAGCAACACAGGGGATTTGGCTGGGCACTTGTCCCAAAAGTGGTGACAC	5517
Qy	1021	GGTCGGTTCCTGTGATAGAGAACTTGACACCTCATCTGCTATAGAACTGACCTTAGATTT	1080
Db	5518	GGTCGGTTCCTGTGATAGAGAACTTGACACCTCATCTGCTATAGAACTGACCTTAGATTT	5577
Qy	1081	ATATTGTACAAGAAATAGTAACGTTCCCTATGTCCCTGGTATTTATTTCTCTGCTTGAGCGG	1140

Db	5578	ATATTGTACAAGAAATAGTAACGTTCCCTATGTCCCTGGTATTTATTTCTCTGCTTGAGCGG	5637
Qy	1141	CAATACGTCGGCTGTATGTACTCAAGACCGAAGCGGCACTTACTACACCATACATGAC	1200
Db	5638	CAATACGTCGGCTGTATGTACTCAAGACCGAAGCGGCACTTACTACACCATACATGAC	5697
Qy	1201	TATCAAAAGGTTCACTCATGCCAACTGCAAGATGACAAATGTAGATGTGTAAACCCCCC	1260
Db	5698	TATCAAAAGGTTCACTCATGCCAACTGCAAGATGACAAATGTAGATGTGTAAACCCCCC	5757
Qy	1261	GGGTATCATATCGCAAAAATATGGAAGACCGGTGTCTCTAAATAGATAAAACAATCATGCAA	1320
Db	5758	GGGTATCATATCGCAAAAATATGGAAGACCGGTGTCTCTAAATAGATAAAACAATCATGCAA	5817
Qy	1321	TGTTTTATCCTTAGGGCGGGATAACTTTAAGGCTCAGTGGGGAATTCGATGTAACTTATCA	1380
Db	5818	TGTTTTATCCTTAGGGCGGGATAACTTTAAGGCTCAGTGGGGAATTCGATGTAACTTATCA	5877
Qy	1381	GAAGAATATCTCAATAAAGATTTCTCAAGTAAATAAACAAGGCAATCTTTGATATCTCAAC	1440
Db	5878	GAAGAATATCTCAATAAAGATTTCTCAAGTAAATAAACAAGGCAATCTTTGATATCTCAAC	5937
Qy	1441	TGAGCTTTGGGAATGTCAACAACCTCGATCAGTAAATGTCTTTGAATPAAGTTAGAGGAAAGCAA	1500
Db	5938	TGAGCTTTGGGAATGTCAACAACCTCGATCAGTAAATGTCTTTGAATPAAGTTAGAGGAAAGCAA	5997
Qy	1501	CAGAAACTAGACAAAGTCAATGTCAAACTGACTAGACATCTGCTCTCATTTACCTTATAT	1560
Db	5998	CAGAAACTAGACAAAGTCAATGTCAAACTGACTAGACATCTGCTCTCATTTACCTTATAT	6057
Qy	1561	CGTTTTGACTATCATATCTCTTTGTTTTGGTATACCTTAGCCTGATTCTAGCATGCTACCT	1620
Db	6058	CGTTTTGACTATCATATCTCTTTGTTTTGGTATACCTTAGCCTGATTCTAGCATGCTACCT	6117
Qy	1621	AATGTAACAAGCAAAAGGCGCAACAAAGACCTTTATTTAGGCTTGGGAATAATACTCTAG	1680
Db	6118	AATGTAACAAGCAAAAGGCGCAACAAAGACCTTTATTTAGGCTTGGGAATAATACTCTAG	6177
Qy	1681	TCAGATGAGGCGCACTACAAAATGTGAACACAGATGAGGACGAAAGTTTCCCTAATAG	1740
Db	6178	TCAGATGAGGCGCACTACAAAATGTGAACACAGATGAGGACGAAAGTTTCCCTAATAG	6237
Qy	1741	TAATTTGTGTGAAAGTTCTGCTAGTCTGCTCAGTTCAGAGAGTTTAAGAAAAAATACCGGT	1800
Db	6238	TAATTTGTGTGAAAGTTCTGCTAGTCTGCTCAGTTCAGAGAGTTTAAGAAAAAATACCGGT	6297
Qy	1801	TGTAGATGACCAAGGACGATATA CGGGTGA GAA CGGTGA GAA CGGTGA GAGAGCGCCCTCAATTGC	1860
Db	6298	TGTAGATGACCAAGGACGATATA CGGGTGA GAA CGGTGA GAA CGGTGA GAGAGCGCCCTCAATTGC	6357
Qy	1861	GAGCCAGGCTTCAACACCTCCGTTCTACCGCTTCA CCGCAACAGTCCCTCAATCATGGAC	1920
Db	6358	GAGCCAGGCTTCAACACCTCCGTTCTACCGCTTCA CCGCAACAGTCCCTCAATCATGGAC	6417
Qy	1921	CGCGCGTTAGCCCAAGTTCGGTTAGAGAAATGATGAAGAGAGGCAAAAAATACATGGCGC	1980
Db	6418	CGCGCGTTAGCCCAAGTTCGGTTAGAGAAATGATGAAGAGAGGCAAAAAATACATGGCGC	6477
Qy	1981	TTGATATTCGGATTCGAAATCTTATTTAA CAGTAGTGACCTTGGCTATATCTGTAGCC	2040
Db	6478	TTGATATTCGGATTCGAAATCTTATTTAA CAGTAGTGACCTTGGCTATATCTGTAGCC	6537
Qy	2041	TCCCTTTTATATAGCATGGGGCTAGCACACCTTAGCGATCTTTGTAGGCAATCCGATAGG	2100
Db	6538	TCCCTTTTATATAGCATGGGGCTAGCACACCTTAGCGATCTTTGTAGGCAATCCGATAGG	6597
Qy	2101	ATTTCCAGGGCAGAGAAAAAGATTATCTACTACCTTGGTTCCAAATCAAGATGTAGTAGAT	2160
Db	6598	ATTTCCAGGGCAGAGAAAAAGATTATCTACTACCTTGGTTCCAAATCAAGATGTAGTAGAT	6657
Qy	2161	AGGATATATAAGCAAGTGGCCCTTGAGTCTCGTTGGCATTTGTTAAATCTGAGACACA	2220

6658 AGGATATATAAGCAAGTGGCCCTTGAGTCTCCGTTGGCATTTGTTAAATACCTAGACACCA 6717
2221 ATTATGAACCGAATAACATCTCTCTTATCAGATTAATGAGCTGCGAAACAAACAGTGGG 2280
6718 ATTATGAACCGAATAACATCTCTCTTATCAGATTAATGAGCTGCGAAACAAACAGTGGG 6777
2281 TGGGGGGCACCTATCCATGACCCAGATTAATATAGGGGGATAGGCAAGAACTCATTTGTA 2340
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2341 GATGATGCTAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2400
6838 GATGATGCTAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6897
2401 ATCCCGGGCTACTACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2460
6898 ATCCCGGGCTACTACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6957
2461 ACCATTACTGCTACACCCATAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2520
6958 ACCATTACTGCTACACCCATAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 7017
2521 TATCAGTATTTAGCATTGCTGCTCGGACATCTGCAACAGGAGGGTATCTTTCT 2580
7018 TATCAGTATTTAGCATTGCTGCTCGGACATCTGCAACAGGAGGGTATCTTTCT 7077
2581 ACTTCGGTTCATCAACCTGGAGACACCCAAAATCGAAAGTCTTCAGTGTGAGTGCA 2640
7078 ACTTCGGTTCATCAACCTGGAGACACCCAAAATCGAAAGTCTTCAGTGTGAGTGCA 7137
2641 ACTTCGGTTCATCAACCTGGAGACACCCAAAATCGAAAGTCTTCAGTGTGAGTGCA 2700
7138 ACTTCGGTTCATCAACCTGGAGACACCCAAAATCGAAAGTCTTCAGTGTGAGTGCA 7197
2701 AACTCAGCTGCTCCATCAGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2760
7198 AACTCAGCTGCTCCATCAGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2820
2761 GAAAGGACCTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2880
7258 GAAAGGACCTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 7317
2821 GGGGGTGTATTTTATGACAGCGCGGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2880
7318 GGGGGTGTATTTTATGACAGCGCGGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 7377
2881 AATTCAACCTGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2940
7378 AATTCAACCTGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 7437
2941 ACATGCCAGATGACAGACTACAGATTCGAATGGCCAGTCTTCGTATAGCCCTGGA 3000
7438 ACATGCCAGATGACAGACTACAGATTCGAATGGCCAGTCTTCGTATAGCCCTGGA 7497
3001 CGGTTTGGTGGAAACCGATACAGAGCTATCTTATCTATCAAGGTTCAACATCCTTA 3060
7498 CGGTTTGGTGGAAACCGATACAGAGCTATCTTATCTATCAAGGTTCAACATCCTTA 7557
3061 GGGGAAGCCGGTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3120
7558 GGGGAAGCCGGTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 7617
3121 AGAATTCACAGTAGGACATCTCATTTCTGATCAACGAGGTTCTATCATCTTCTCT 3180
7618 AGAATTCACAGTAGGACATCTCATTTCTGATCAACGAGGTTCTATCATCTTCTCT 7677
3181 CCGCGTTTATTTATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3240
7678 CCGCGTTTATTTATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 7737
3241 ACATTCAATGCTTCACTCGGCCAGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3300
7738 ACATTCAATGCTTCACTCGGCCAGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 7797

Qy 3301 AACTCGTGTCTTACTGAGTCTATACAGATCCATATCCCTAATCTTCTATAGAAACC 3358
Db 7798 AACTCGTGTCTTACTGAGTCTATACAGATCCATATCCCTAATCTTCTATAGAAACC 7855

RESULT 5

ADM78414
ID ADM78414 standard; cDNA; 5292 BP.
XX
AC ADM78414;
XX
DT 03-JUN-2004 (first entry)
XX
DE Newcastle disease virus recombinant cDNA #10.
XX
KW Newcastle disease virus; T7 RNA polymerase; H5p-2 cell; influenza virus;
KW infectious bursal disease virus; rotavirus; infectious bronchitis virus;
KW chicken anaemia virus; Marek's disease virus; avian Leukosis virus;
KW avian adenovirus; avian pneumovirus;
KW severe acute respiratory syndrome-causing virus; SARS;
KW human respiratory syncytial virus; human immunodeficiency virus;
KW hepatitis virus; measles virus; mumps virus; antiviral; ss.
XX
OS Newcastle disease virus.
XX
FN US2003224017-A1.
XX
PD 04-DEC-2003.
XX
PF 19-MAY-2003; 2003US-00440419.
XX
PR 05-MAY-2000; 2000WO-US0006700.
PR 06-MAR-2002; 2002US-00926431.
PR 17-MAY-2002; 2002US-0381462P.
XX
PA (SAMA/) SAMAL S K.
PA (HUAN/) HUANG Z.
XX
PI Samal SK, Huang Z;
XX
PI WPI; 2004-051891/05.
XX
PS Novel antigenomic RNA of Newcastle disease virus having NP, P, M, F, HN,
L genes and foreign nucleotide complex inserted before NP gene, between
P, M genes and/or between HN, L genes, useful for producing vaccine
vector.
XX
PS Example 3; Page 12-14; 41pp; English.
XX
CC The invention relates to an antigenomic RNA of Newcastle disease virus
having NP, P, M, F, HN and L genes in the 5'-3' direction, with foreign
nucleotide complexes inserted between genes. The invention also relates
to cDNA related to the RNA, a plasmid comprising the cDNA, a cell
comprising the RNA, cDNA or plasmid, a method of preparing the RNA and a
recombinant Newcastle disease virus comprising the RNA. The RNA is useful
for producing a recombinant Newcastle disease virus by providing cells
capable of synthesizing T7 RNA polymerase, transfecting the cells with a
plasmid comprising cDNA or a protein of interest to obtain transfect
cells in a medium and isolating Newcastle disease virus from a
supernatant of the medium, where the cells capable synthesizing T7 RNA
polymerase are from a cell line expressing T7 RNA polymerase or plant
cells, mammalian cells, avian cells or HEP-2 cells infected with a
vaccinia virus that can synthesize T7 RNA polymerase. The recombinant
virus is useful for vaccinating an avian animal against Newcastle disease
or an avian pathogen chosen from influenza virus, infectious bursal
disease virus, rotavirus, infectious bronchitis virus, chicken anaemia
virus, Marek's disease virus, avian Leukosis virus, avian adenovirus and
avian pneumovirus, where the avian animal is in need of the immunisation,
which involves administering the recombinant virus to the avian animal,
where the open reading frame of the foreign gene encodes an immunogenic
protein of the avian pathogen against which the avian animal is
immunized. The recombinant virus is also useful for immunising a mammal

CC	against a non-avian pathogen such as severe acute respiratory syndrome-
CC	causing virus (SARS virus), human respiratory syncytial virus, human
CC	immunodeficiency virus, hepatitis virus, measles virus or mumps virus.
CC	This sequence represents Newcastle disease virus recombinant cDNA of the
XX	invention.
SQ	Sequence 5292 BP; 1574 A; 1207 C; 1186 G; 1324 T; 0 U; 1 Other;
	Query Match 96.5%; Score 3240.4; DB 12; Length 5292;
	Best Local Similarity 99.7%; Pred. No. 0;
	Matches 3267; Conservative 1; Mismatches 8; Indels 2; Gaps 2;
Qy	82 TATGATCGTCACTATCCGGGTGGCGCTGGCACTGAGTTGCATCTGTCCGGCAAACTCCAT 141
Db	1 TATGATCGTCACTATCCGGGTGGCGCTGGTACTGAGTTGCATCTGTCCGGCAAACTCCAT 60
Qy	142 TGAATGGCAGGCTCTTGACGTGCGAGAAATGTGGTTACAGGAGACAAAGCCGTCAACAT 201
Db	61 TGAATGGCAGGCTCTTGACGTGCGAGAAATGTGGTTACAGGAGACAAAGCCGTCAACAT 120
Qy	202 ATACACCTCATCCAGACAGATCAATCATAGTTAAGCTCTCCCGAATCTGCCAAGGA 261
Db	121 ATACACCTCATCCAGACAGATCAATCATAGTTAAGCTCTCCCGAATCTGCCAAGGA 180
Qy	262 TAAGGAGGCATGTGCGAAAGCCCTTGGATGCATACAAACAGACATTTGACCACTTTGCT 321
Db	181 TAAGGAGGCATGTGCGAAAGCCCTTGGATGCATACAAACAGACATTTGACCACTTTGCT 240
Qy	322 CACCCCTTTGGTGACTCTATCCGTAGGATCAAGAGTCTGTGACTACATCTGGAGGGG 381
Db	241 CACCCCTTTGGTGACTCTATCCGTAGGATCAAGAGTCTGTGACTACATCTGGAGGGG 300
Qy	382 GAGACAGGGGCGCTTATAGCGGCATTTATGGCGGTGTGGCTCTTGGGTTGCCAAGTGC 441
Db	301 GAGACAGGGGCGCTTATAGCGGCATTTATGGCGGTGTGGCTCTTGGGTTGCCAAGTGC 360
Qy	442 CGCAAAATAACAGCGCGCGAGCTCTGATACAGCCAAACAAATGCTGCCAACAATCCT 501
Db	361 CGCAAAATAACAGCGCGCGAGCTCTGATACAGCCAAACAAATGCTGCCAACAATCCT 420
Qy	502 CCGACTTTAAAGAGAGCAATTCGCGCAACCAATGAGGCTGTGCATGAGGTCTCTGACGGATT 561
Db	421 CCGACTTTAAAGAGAGCAATTCGCGCAACCAATGAGGCTGTGCATGAGGTCTCTGACGGATT 480
Qy	562 ATCCCACTAGCAGTGCAGTTGGGAAGATGCAGCAGTTTGTAAATGACCAATTTAATAA 621
Db	481 ATCCCACTAGCAGTGCAGTTGGGAAGATGCAGCAGTTTGTAAATGACCAATTTAATAA 540
Qy	622 AACAGCTCAGGAATTAGACTGCAATCAAAATTTGCACAGCAAGTTGGTGTAGAGCTCAACCT 681
Db	541 AACAGCTCAGGAATTAGACTGCAATCAAAATTTGCACAGCAAGTTGGTGTAGAGCTCAACCT 600
Qy	682 GTACCTAACCGAATTGACTACAGTATTCGACCAACAAATCACTTCACCTGCTTTAAACAA 741
Db	601 GTACCTAACCGAATTGACTACAGTATTCGACCAACAAATCACTTCACCTGCTTTAAACAA 660
Qy	742 GCTGACTATTTCAGGCACCTTACAAATCTAGCTGGTGGAAATATGGAATTACTTTTACTAA 801
Db	661 GCTGACTATTTCAGGCACCTTACAAATCTAGCTGGTGGAAATATGGAATTACTTTTACTAA 720
Qy	802 GTTAGGTGTAGGGAACCAATCAACTCAGCTCATTAATCGGTAGCGGCTTAATCAACCGTAA 861
Db	721 GTTAGGTGTAGGGAACCAATCAACTCAGCTCATTAATCGGTAGCGGCTTAATCAACCGTAA 780
Qy	862 CCCTATTCTATACGACTCAGACTCAACTCTTGGGTATACAGGTAACTCTACCTTCAGT 921
Db	781 CCCTATTCTATACGACTCAGACTCAACTCTTGGGTATACAGGTAACTCTACCTTCAGT 840
Qy	922 CGGGAACCTAAATAATATGGTGCACCTACTTGGAAACCTTATCCGTAAAGCAACACAG 981
Db	841 CGGGAACCTAAATAATATGGTGCACCTACTTGGAAACCTTATCCGTAAAGCAACACAG 900
Qy	982 GGGATTTGCGTGGCACTTTGTCCCAAAAGTGGTGACACAGTCTGGTTCTGTGTAGAGA 1041

Db	901 GGGATTTGCTCGGCACCTTGTCCTCCAAAAGTGGTGACACAGGTCGGTCTCTGTGTAGAGA 960
Qy	1042 ACTTGACACTCATCTACTGTATAGAAACTGACTTAGATTTTATTTGTACAAAGATAGTAAC 1101
Db	961 ACTTGACACTCATCTACTGTATAGAAACTGACTTAGATTTTATTTGTACAAAGATAGTAAC 1020
Qy	1102 GTTCCCTATGTCCCTGGTATTTATTCCTGCTTGAGCGGCAATACATCGCGCTGTATGTA 1161
Db	1021 GTTCCCTATGTCCCTGGTATTTATTCCTGCTTGAGCGGCAATACATCGCGCTGTATGTA 1080
Qy	1162 CTCAAAAGCCGAAGGCGCACTTACTACACCATACATGACTATCAAAAGTTCAAGTCATCGC 1221
Db	1081 CTCAAAAGCCGAAGGCGCACTTACTACACCATACATGACTATCAAAAGTTCAAGTCATCGC 1140
Qy	1222 CAACTCCAGATGACAAACATGTAGATGTGTAAACCCCGGGTATCATATCGCAAACTA 1281
Db	1141 CAACTCCAGATGACAAACATGTAGATGTGTAAACCCCGGGTATCATATCGCAAACTA 1200
Qy	1282 TGGAGAACCGTCTCTCTAATAGATAAAACAATCATGCAATGTTTTATCCTTAGCGGGAT 1341
Db	1201 TGGAGAACCGTCTCTCTAATAGATAAAACAATCATGCAATGTTTTATCCTTAGCGGGAT 1260
Qy	1342 AACTTTAAGGCTCAGTGGGAAATTCGATGTAACTTATCAGAAAGATATCTCAATACAAGA 1401
Db	1261 AACTTTAAGGCTCAGTGGGAAATTCGATGTAACTTATCAGAAAGATATCTCAATACAAGA 1320
Qy	1402 TTCTCAAGTAATTAACAGGCAATCTTGATATCTCACTGAGCTTTGGGAATGTCAACAA 1461
Db	1321 TTCTCAAGTAATTAACAGGCAATCTTGATATCTCACTGAGCTTTGGGAATGTCAACAA 1380
Qy	1462 CTCGATCAGTAAATGCTTTGAATAAGTTAGAGAAAGCAACAGAAAAGTACAGAAAGTCAA 1521
Db	1381 CTCGATCAGTAAATGCTTTGAATAAGTTAGAGAAAGCAACAGAAAAGTACAGAAAGTCAA 1440
Qy	1522 TGTCAAACTGACTAGCACATCTGCTCTCATTTACTATATCGTTTGTGACTATCATATCTCT 1581
Db	1441 TGTCAAACTGACCAGCACATCTGCTCTCATTTACTTATACCTATATCGTTTGTGACTATCATATCTCT 1500
Qy	1582 TGTTTTGTGTATCTTAGCCCTGATTTCTAGCATGTCTAATGTACAGCAAGAAAGGGCA 1641
Db	1501 TGTTTTGTGTATCTTAGCCCTGATTTCTAGCATGTCTAATGTACAGCAAGAAAGGGCA 1560
Qy	1642 ACAAAAACCTTATTTATGCTTTGGGAATTAATCTCTAGATCAGATCAGAGCCACTCAAA 1701
Db	1561 ACAAAAACCTTATTTATGCTTTGGGAATTAATCCCTAGATCAGATCAGAGCCACTCAAA 1620
Qy	1702 AATGTGAACACAGATGAGGAACGAAGGTTTCCCTAATAGTAAATTTGTGTAAAGTTCTGG 1761
Db	1621 AATGTGAACACAGATGAGGAACGAAGGTTTCCCTAATAGTAAATTTGTGTAAAGTTCTGG 1680
Qy	1762 TAGTCTGTGAGTTACAGAGATTTAAGAAAAAACTACCGGTTGTAGATGACCAAGGAGAT 1821
Db	1681 TAGTCTGTGAGTTACAGAGATTTAAGAAAAAACTACCGGTTGTAGATGACCAAGGAGAT 1740
Qy	1822 ATACGGGTAGACGGTAAGAGAGCGCGCCCTCAATTTGCGAGCCAGGCTTCAACACTCC 1881
Db	1741 ATACGGGTAGACGGTAAGAGAGCGCGCCCTCAATTTGCGAGCCAGGCTTCAACACTCC 1800
Qy	1882 GTTCTTACCGCTTCAACCGACAAACAGTCTCTCAATCATGGACCGCGCTTAGCCAAAGTTGG 1941
Db	1801 GTTCTTACCGCTTCAACCGACAAACAGTCTCTCAATCATGSAACCGCGCTTAGCCAAAGTTGG 1860
Qy	1942 TTAGAAATGATGAAAGAGAGGCAAAAAATATATGGCGCTTGATATTCGGATTTGCAATC 2001
Db	1861 TTAGAAATGATGAAAGAGAGGCAAAAAATATATGGCGCTTGATATTCGGATTTGCAATC 1920
Qy	2002 TTATTTCTTAACAGTACTGACCTTGGCTATATCTGTAGCTCCCTTTTATATACATGGGG 2061
Db	1921 TTATTTCTTAACAGTACTGACCTTGGCTATATCTGTAGCTCCCTTTTATATAGCATGGGG 1980
Qy	2062 GCTAGCACACCTAGCGCATCTTGTAGGCATACCGACTAGGATTTCCAGGGCAGAAAGAAAG 2121

Db 1981 GCTAGCACCTAGCGATCTTGTAGGCATACCGACTAGGATTTCCAGGCGAGAGAAAG 2040
Qy 2122 ATTACATCTACATTGGTTCCAAATCAAGATGTAGTAGGATATATAAGCAAGTGGCC 2181
Db 2041 ATTACATCTACATTGGTTCCAAATCAAGATGTAGTAGGATATATAAGCAAGTGGCC 2100
Qy 2182 CTTGAGTCTCGGTTGGCAATCTTAAATACTAGACCAAAATATATGAAAGCAATACATCT 2241
Db 2101 CTTGAGTCTCGGTTGGCAATCTTAAATACTAGACCAAAATATATGAAAGCAATACATCT 2160
Qy 2242 CTCTCTTATCAGATTATAGGAGCTGCAAAACACAGTGGTGGGGGCAACCTTATCCATGAC 2301
Db 2161 CTCTCTTATCAGATTATAGGAGCTGCAAAACACAGTGGTGGGGGCAACCTTATCCATGAC 2220
Qy 2302 CCAGATTATATAGGGGGGATAGGCAAGAACTCATTTGTAGATGATGCTAGTGTGTACACA 2361
Db 2221 CCAGATTATATAGGGGGGATAGGCAAGAACTCATTTGTAGATGATGCTAGTGTGTACACA 2280
Qy 2362 TCATTCTATCCCTCTGCATTTTCAGAACATCTGAATTTTATCCGGCGCTACTACAGGA 2421
Db 2281 TCATTCTATCCCTCTGCATTTTCAGAACATCTGAATTTTATCCGGCGCTACTACAGGA 2340
Qy 2422 TCAGGTTGCACCTCGAATAACCTCATTTGACATGAGTGTACCCATTACTGTACACCCAT 2481
Db 2341 TCAGGTTGCACCTCGAATAACCTCATTTGACATGAGTGTACCCATTACTGTACACCCAT 2400
Qy 2482 AATGTAATATGTCTGGATGACAGATCACTCAATTCATATCATGATTTTAGCACTTGGT 2541
Db 2401 AATGTAATATGTCTGGATGACAGATCACTCAATTCATATCATGATTTTAGCACTTGGT 2460
Qy 2542 GTGCTCCGGACATCTGCACAGGAGGGTATCTTTTCTACTCTGCGTCCATCAACCTG 2601
Db 2461 GTGCTCCGGACATCTGCACAGGAGGGTATCTTTTCTACTCTGCGTCCATCAACCTG 2520
Qy 2602 GACGACACCCAAATCGGAAGTCTTGAGTGTGAGTGCAACTCCCTCGGTTGTGATATG 2661
Db 2521 GACGACACCCAAATCGGAAGTCTTGAGTGTGAGTGCAACTCCCTCGGTTGTGATATG 2580
Qy 2662 CTGTGCTCGAAGTCAAGGACAGAGAGAAAGATTATTAATCAGCTGTCCCTACCGGG 2721
Db 2581 CTGTGCTCGAAGTCAAGGACAGAGAGAAAGATTATTAATCAGCTGTCCCTACCGGG 2640
Qy 2722 ATGTACATGGAGGTTAGGTTTGCACGGCCAGTACCAG-AAAAGNCTTAGATGTAC 2780
Db 2641 ATGTACATGGAGGTTAGG-TCGACGGCCAGTACCAGAAAGGACCTTAGATGTAC 2699
Qy 2781 AACATTATTTCGGGACTCGGTGGCCAACTACCCAGGAGTAGGGGTGGATCTTTTATTGA 2840
Db 2700 AACATTATTTCGGGACTCGGTGGCCAACTACCCAGGAGTAGGGGTGGATCTTTTATTGA 2759
Qy 2841 CAGCCGGTATGGTTCTCAGTCTACGGAGGTTTAAACCCCAATTACCCAGTGCACCTGT 2900
Db 2760 CAGCCGGTATGGTTCTCAGTCTACGGAGGTTTAAACCCCAATTACCCAGTGCACCTGT 2819
Qy 2901 ACAGAAAGGAAATATGTGATATACAGCGATACATGACACATGCCAGATGAGCAGA 2960
Db 2820 ACAGAAAGGAAATATGTGATATACAGCGATACATGACACATGCCAGATGAGCAGA 2879
Qy 2961 CTACAGATTGCAATGGCCAAAGTCTTCTGTAAGCTCGGCGTTTGGTGGAAACGCAT 3020
Db 2880 CTACAGATTGCAATGGCCAAAGTCTTCTGTAAGCTCGGCGTTTGGTGGAAACGCAT 2939
Qy 3021 ACAGCAGGCTATCTTATCTATCAAGGTTGTCACATCTCTTAGGCGAAGACCCGGTACTGAC 3080
Db 2940 ACAGCAGGCTATCTTATCTATCAAGGTTGTCACATCTCTTAGGCGAAGACCCGGTACTGAC 2999
Qy 3081 TGTACCGCCCAACACAGTCACTCATGGGGGCGAAGGCAAGATTCTCAGATAGGGAC 3140
Db 3000 TGTACCGCCCAACACAGTCACTCATGGGGGCGAAGGCAAGATTCTCAGATAGGGAC 3059
Qy 3141 ATCTCATTTCTGTATCAACGAGGTCATCATCTTCTCCCGGTTATTATATCTTAT 3200
Db 3060 ATCTCATTTCTGTATCAACGAGGTCATCATCTTCTCCCGGTTATTATATCTTAT 3119

Qy 3201 GACAGTCAGCAACAAACAGCCACTCTTCATAGTCCCTTATATCATTCATGCTTCACTCG 3260
Db 3120 GACAGTCAGCAACAAACAGCCACTCTTCATAGTCCCTTATATCATTCATGCTTCACTCG 3179
Qy 3261 GCCAGGTAGTATCCCTTCCAGGCTTCAGCAAGATGCCCAACTCGTGTGTACTGGAGT 3320
Db 3180 GCCAGGTAGTATCCCTTCCAGGCTTCAGCAAGATGCCCAACTCGTGTGTACTGGAGT 3239
Qy 3321 CTATACAGATCCATATCCCTTAATCTTCTATAGAAACC 3358
Db 3240 CTATACAGATCCATATCCCTTAATCTTCTATAGAAACC 3277

RESULT 6

AA70261
ID AA70261 standard; cDNA; 3825 BP.
XX AA70261;
AC
XX
XX 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 03-APR-1991 (first entry)
XX
DE
XX Sequence of Newcastle Disease Virus (NDV) F gene and HN gene.
XX Epitope; probe; diagnosis; ss.
XX
OS Newcastle disease virus.

Key Location/Qualifiers
misc_feature 1..1792
/tag= a
/label= F gene
CDS 47..1708
/tag= c
/product= "F"
/note= "AAP70176"
misc_feature 1795..3825
/tag= b
/label= HN gene
CDS 1915..3648
/tag= d
/product= "HN"
/note= "AAP70843"

EP227414-A.

01-JUL-1987.

16-DEC-1986; 86EP-00309804.

18-DEC-1985; 85GB-000311147.

14-APR-1986; 86GB-00009037.

15-JUL-1986; 86US-00885765.

(NATR) NAT RES DEV CORP.

Bingham RW, Chambers P, Emmerson PT, Millar NS;

WPI; 1987-179630/26.

P-PSDB; AAP70176, AAP70843.

Newcastle disease virus gene clones - comprise polynucleotide(s) encoding the HN and/or F protein of Newcastle disease virus RNA.

Example; Page 11-16; 22pp; English.

An artificial polynucleotide encoding an HN and/or F polypeptide of Newcastle Disease Virus (NDV) DNA, a bioprecursor of the polypeptide, or an epitopic portion of the polypeptide or an artificial nucleotide complementary to the polynucleotide are claimed. The polynucleotides are useful for preparing a probe for extracting similar genes from a gene

CC library or for identifying the presence of NDV virions in a sample obtd.
CC from poultry. (Updated on 25-MAR-2003 to correct PA field.) (Updated on
CC 27-AUG-2003 to correct OS field.)

Sequence 3825 BP; 1122 A; 898 C; 856 G; 949 T; 0 U; 0 Other;

Query Match	95.2%	Score 3196.4;	DB 1;	Length 3825;
Best Local Similarity	97.0%;	Pred. NO. 0;		
Matches 3257;	Conservative	0;	Mismatches 101;	Indels 0;
Gaps 0;				

Qy	1	ACGGGTAGAGATTCTGGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACC	60
Db	1		
Qy	61	TTCTACCAAGAACCCAGCACCTATGATGCTGACTATCCGGGTTGGGCTGGCAGCTGAGTTG	120
Db	61		
Qy	121	CATCTGTCCGCAAACTCCATTGATGGCAGGCCCTCTTGCAGCTGCAGGAATTTGGTGTAC	180
Db	121		
Qy	181	AGGAGACAAAGCCGTCAACATATATACA CTTCAATCCAGACAGGATCAATCATAGTTAAAGCT	240
Db	181		
Qy	241	CCTCCCGAATCTGCCCAAGGATAGGAGGCATGTCGNAAGCCCTTGGATGCATCAAA	300
Db	241		
Qy	301	CAGGACATTTGACCACTTTGCTCACCCCCCTTTGGTGACTCTATCCGTAGGATACAAAGATC	360
Db	301		
Qy	361	TGTGACTACATCTGGAGGAGGAGACAGAAACGCTTTATAGCGCCATTTATTGGCGGTGT	420
Db	361		
Qy	421	GGCTCTTGGGGTTGCAACTGCGGCACAAATACAGCGCGCCAGCTCTGATACAAAGCCAA	480
Db	421		
Qy	481	ACAAAATGCTGCCCAACTCTCTCCGACTTTAAAGAGAGCATTGCCCGCAACCAATGAGGCTGT	540
Db	481		
Qy	541	GCATGAGGTCACTGACGGATTATCGCAACTAGCAGTGGCAGTTGGGAAGATGCGACAGTT	600
Db	541		
Qy	601	TGTTAATGACCAATTTAATAAAACAGCTCAGGAATTAGATGTCATCAAAATTTGCACAGCA	660
Db	601		
Qy	661	AGTTGGTGTAGAGCTCAACCTGTACCTAAACCGAATTGACTACAGTATTTCGGACCACAAAAT	720
Db	661		
Qy	721	CACCTCACCTGCTTTTAAACAAAGCTGACTATTTACGGCACTTTTACAAATCTAGCTGGTGGAAA	780
Db	721		
Qy	781	TATGGATTACTTATTTGACTAAGTTAGGTGATGGGAA CAAATCAACTCAGCTCATTAATCGG	840
Db	781		
Qy	841	TAGCGGCTTAATCACCGGTAAACCCCTATTCTATACGACTCACAGACTCAA CTTCTTGGGTAT	900
Db	841		
Qy	901	ACAGGTAACTCTA CTTCTCAGTCGGGAAACCTTAATAATATGCGTGCCCACTTCTTGGAAAC	960
Db	901		

2041 TCCCTTTTATATAGCATGGGGCTAGCACACCTAGCGATCTTGTAGGCATACCCAGTGG 2100
Db |||||||
2041 TCCCTTGTATATAGCATGGGGCTAGCACACCTAGCGACCTTGTAGGCATACCCAGCAGG 2100
Qy |||||||
2101 ATTTCAGGGCAGAGAAAGATTACATCTACACTTGGTTCCAAATCAAGATGTAGTAGAT 2160
Db |||||||
2101 ATTTCAGGGCAGAGAAAGATTACATCTGCACCTTGGTTCCAAATCAAGATGTAGTAGAT 2160
Qy |||||||
2161 AGGATATATAAGCAAGTGGCCCTTGAAGTCTCCGTTGGCAATTTAAATATCTGAGACACCA 2220
Db |||||||
2161 AGGATATATAAGCAAGTGGCCCTTGAAGTCTCCGTTGGCAATTTAAATATCTGAGACACCA 2220
Qy |||||||
2221 ATTATGAACCAATAACATCTCTCTATCAGATTAATGAGCTGCAACCAACAGTGGG 2280
Db |||||||
2221 ATTATGAACCAATAACATCTCTCTATCAGATTAATGAGCTGCGCAACAGCGGG 2280
Qy |||||||
2281 TGGGGGCGACCTATCCATGACCCAGATTATATAGGGGGATAGGCAAGAACTCATTTGTA 2340
Db |||||||
2281 TGGGGGCGACCTATCCATGACCCAGATTATATCGGGGGATAGGCAAGAACTCATTTGTA 2340
Qy |||||||
2341 GATGATCTAGTGTGATGTACATCATCTTATCCCTCTGCAATTCAGAACATCTCAATTTT 2400
Db |||||||
2341 GATGATCTAGTGTGATGTACATCATCTTATCCCTCTGCAATTCAGAACATCTCAATTTT 2400
Qy |||||||
2401 ATCCCGGCGCTACTACAGGATCAGGTGCTGCAATACCTCATTTGATCATGAGTGT 2460
Db |||||||
2401 ATCCCGGCGCTACTACAGGATCAGGTGCTGCAATACCTCATTTGATCATGAGTGT 2460
Qy |||||||
2461 ACCATTACTGCTACACCCCAATGTAATATGCTGATGTCAGATGTCAGATCACTACATCA 2520
Db |||||||
2461 ACCATTACTGCTACACCCCAATGTAATATGCTGATGTCAGATGTCAGATCACTACATCA 2520
Qy |||||||
2521 TATCAGTATTTAGCACTTGTGTGCTCCGGACATCTGCAACAGCGAGGGTATTTCTTTCT 2580
Db |||||||
2521 TATCAGTATTTAGCACTTGTGTGCTCCGGACATCTGCAACAGCGAGGGTATTTCTTTCT 2580
Qy |||||||
2581 ACTCTGGTTCATACACTGGAGACACACCAAAATCGGAAGTCTTGCAGTGTGAGTGCA 2640
Db |||||||
2581 ACTCTGGTTCATACACTGGAGTGCAGACAGCCAAAATCGGAAGTCTTGCAGTGTGAGTGCA 2640
Qy |||||||
2641 ACTCCCGTGGTGTGATATGCTGTCGGAAGTCTGCAAGTCTGCGAGCAGAGGAGAGATTAT 2700
Db |||||||
2641 ACTCCCGTGGTGTGATATGCTGTCGGAAGTCTGCAAGTCTGCGAGCAGAGGAGAGATTAT 2700
Qy |||||||
2701 AACTCAGCTGTCCCTACGCGATCGTATCGGAGGTAGGTTGCGACGGCCAGTACCAC 2760
Db |||||||
2701 AACTCAGCTGTCCCTACGCTGATGCGCATGGGAGTTAGGTTGCGACGGCCATACCAC 2760
Qy |||||||
2761 GAAAGGACCTAGACGTACAACTATTTGCGGACCTGGGTGGCCAACTACCCAGGAGTA 2820
Db |||||||
2761 GAAAGGACCTAGACGTACAACTATTTGCGGACCTGGGTGGCCAACTACCCAGGAGTA 2820
Qy |||||||
2821 GGGGGTGGATCTTTTATGACAGCGCGGTATGTTCTCAGTCTACGAGGGTTAAACCC 2880
Db |||||||
2821 GGGGGTGGATCTTTTATGACAGCGCGGTATGTTCTCAGTCTACGAGGGTGAACCC 2880
Qy |||||||
2881 AATTCAACCGTACCTGTACAGGAGGGAATATGTATATACAGCGATACCAATGAC 2940
Db |||||||
2881 AATTCAACCGTACCTGTACAGGAGGGAATATGTATATACAGCGATACCAATGAC 2940
Qy |||||||
2941 ACATGCCAGATGACGAGACTACAGATTGCGAATGCGCAAGTCTCGTATAGCCCTGGA 3000
Db |||||||
2941 ACATGCCAGATGACGAGACTACAGATCGAATGCGCAAGTCTCGTATAGCCCTGGA 3000
Qy |||||||
3001 CGGTTTGGTGGAAACGATACAGAGCTATCTTATCTATCAAGGTGTCAACATCTTTA 3060
Db |||||||
3001 CGGTTTGGTGGAAACGATACAGAGCTATCTTATCTATCAAGGTGTCAACATCTTTG 3060
Qy |||||||
3061 GGGCAAGACCGGTACTGACTGTACCGCCCAACAGCTCACACTCATGGGGCGGAGGC 3120
Db |||||||
3061 GGGCAAGACCGGTACTGACTGTACCGCCCAACAGCTCACACTCATGGGGCGGAGGC 3120
Qy |||||||
3121 AGAATTCACAGTGGGACATCTCAATTTTGTATCAACGAGGGTGCATCATCTTCTCT 3180

Db |||||||
3121 AGAATTCACAGTGGGACATCTCAATTTTGTATCAGGAGGTGCATCATCTTCTCT 3180
Qy |||||||
3181 CCOCGGTATTATATCTATCTATGACAGTGCAGCAACAAAACAGCCACTCTTTCATAGTCTTAT 3240
Db |||||||
3181 CCOCGGTATTATATCTATCTATGACAGTGCAGCAACAAAACAGCCACTCTTTCATAGTCTTAT 3240
Qy |||||||
3241 ACATTCAATGCTTCACTCGGCCAGGTAGTATCCCTTGCAGGGTTCAGCAAGATGCCCC 3300
Db |||||||
3241 ACATTCAATGCTTCACTCGGCCAGGTAGTATCCCTTGCAGGGTTCAGCAAGATGCCCC 3300
Qy |||||||
3301 AACTCGTGTGTTACTGAGTCTATACAGTCCATATCCCTTAATCTTCTATAGAAACC 3358
Db |||||||
3301 AACTCGTGTGTTACTGAGTCTATACAGTCCATATCCCTTAATCTTCTATAGAAACC 3358
RESULT 7
ADM78418
ID ADM78418 standard; cDNA; 5291 BP.
XX
AC ADM78418;
XX AC
DT 03-JUN-2004 (first entry)
XX
DE Newcastle disease virus recombinant cDNA #14.
XX
KW Newcastle disease virus; T7 RNA polymerase; HEp-2 cell; influenza virus;
KW infectious bursal disease virus; rotavirus; infectious bronchitis virus;
KW chicken anaemia virus; Marek's disease virus; avian Leukosis virus;
KW avian adenovirus; avian pneumovirus;
KW severe acute respiratory syndrome-causing virus; SARS;
KW human respiratory syncytial virus; human immunodeficiency virus;
KW hepatitis virus; measles virus; mumps virus; antiviral; ss.
XX
OS Newcastle disease virus.
XX
PN US2003224017-A1.
XX
PD 04-DEC-2003.
XX
PF 19-MAY-2003; 2003US-00440419.
XX
PR 05-MAY-2000; 2000WO-US0006700.
PR 06-MAR-2002; 2002US-00926431.
PR 17-MAY-2002; 2002US-0381462P.
XX
PA (SAMA/) SAMAL S K.
PA (HUAN/) HUANG Z.
XX
PI Samal SK, Huang Z;
XX
PI
XX
DR WPI; 2004-051891/05.
XX
PT Novel antigenomic RNA of Newcastle disease virus having NP, P, M, F, HN,
PT L genes and foreign nucleotide complex inserted before NP gene, between
PT P, M genes and/or between HN, L genes, useful for producing vaccine
PT vector.
XX
PS Example 3; Page 18-19; 41pp; English.
XX
CC The invention relates to an antigenomic RNA of Newcastle disease virus
CC having NP, P, M, F, HN and L genes in the 5'-3' direction, with foreign
CC nucleotide complexes inserted between genes. The invention also relates
CC to cDNA related to the RNA, a plasmid comprising the cDNA, a cell
CC comprising the RNA, cDNA or plasmid, a method of preparing the RNA and a
CC recombinant Newcastle disease virus comprising the RNA. The RNA is useful
CC for producing a recombinant Newcastle disease virus by providing cells
CC capable of synthesising T7 RNA polymerase, transfecting the cells with a
CC plasmid comprising cDNA or a protein of interest to obtain transfected
CC cells in a medium and isolating Newcastle disease virus from a
CC supernatant of the medium, where the cells capable synthesising T7 RNA
CC polymerase are from a cell line expressing T7 RNA polymerase or plant
CC cells, mammalian cells, avian cells or HEp-2 cells infected with a

CC vaccinia virus that can synthesise T7 RNA polymerase. The recombinant
CC virus is useful for vaccinating an avian animal against Newcastle disease
CC or an avian pathogen chosen from influenza virus, infectious bursal
CC disease virus, rotavirus, infectious bronchitis virus, chicken anaemia
CC virus, Marek's disease virus, avian Leukosis virus, avian adenovirus and
CC avian pneumovirus, where the avian animal is in need of the immunisation,
CC which involves administering the recombinant virus to the avian animal,
CC where the open reading frame of the foreign gene encodes an immunogenic
CC protein of the avian pathogen against which the avian animal is
CC immunized. The recombinant virus is also useful for immunising a mammal
CC against a non-avian pathogen such as severe acute respiratory syndrome-
CC causing virus (SARS virus), human respiratory syncytial virus, human
CC immunodeficiency virus, hepatitis virus, measles virus or mumps virus.
CC This sequence represents Newcastle disease virus recombinant cDNA of the
CC invention.
XX
SQ Sequence 5291 BP; 1565 A; 1202 C; 1186 G; 1332 T; 0 U; 6 Other;

Query Match 72.7%; Score 2441.6; DB 12; Length 5291;
Best Local Similarity 97.0%; Pred. No. 0;
Matches 2486; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

QY 796 GACTAAGTTAGGTGTAGGAGCAATCAACTCAGCTCATTAATCGGTAGCGGCTTAATCAC 855
DB 1 GACTAAGTTAGGTGTAGGAGCAATCAACTCAGCTCATTAATCGGTAGCGGCTTAATCAC 60
QY 856 CGGTAAACCTTATCTATACAGCTCACAGCTCAACTCTTGGGTATACAGTAACTCTACC 915
DB 61 CGGCAACCTTATCTGTACAGCTCACAGCTCAACTCTTGGGTATACAGTAACTCTACC 120
QY 916 TTCAGTCCGGGAACCTAAATAATATGCGTGCCACCTACTTTGGAAACCTTATCCGTAAAGCAC 975
DB 121 TTCAGTCCGGGAACCTAAATAATATGCGTGCCACCTACTTTGGAAACCTTATCCGTAAAGCAC 180
QY 976 AACGAGGGAATTGGCTCGGCACCTGTCCAAAAGTGGTGACACAGCTCGGTTCTGTGAT 1035
DB 181 AACGAGGGAATTGGCTCGGCACCTGTCCAAAAGTGGTGACACAGCTCGGTTCTGTGAT 240
QY 1036 AGAAGAACTTGACACCTCATACTGTATAGAACTGACTTAGATTTATATTGTACAAGAAAT 1095
DB 241 AGAAGAACTTGACACCTCATACTGTATAGAACTGACTTAGATTTATATTGTACAAGAAAT 300
QY 1096 AGTAAAGTTCCTTATGTCCTCGGTATTTATTCCTGTTGAGCGGCAATACTCGGCGCTG 1155
DB 301 AGTAAACATTCCTTATGTCCTCGGTATTTATTCCTGTTGAGCGGCAATACATCGGCGCTG 360
QY 1156 TATGTACTCAAGACCGAAGCGCAGCTTACTACACATACATGACTATCAAGGTTCACT 1215
DB 361 TATGTACTCAAGACCGAAGCGCAGCTTACTACACATACATGACTATCAAGGTTCACT 420
QY 1216 CATCGGCACTGCAAGATGACAACTGTAGATGTGTAAACCCCGGGGTATCATATCGCA 1275
DB 421 CATCGGCACTGCAAGATGACAACTGTAGATGTGTAAACCCCGGGGTATCATATCGCA 480
QY 1276 AAACCTATGGGAAGCCGTGTCTCTAATAGATAAACAATCATGCAATGTTTTATCCTTAGG 1335
DB 481 AAACCTATGGGAAGCCGTGTCTCTAATAGATAAACAATCATGCAATGTTTTATCCTTAGA 540
QY 1336 CGGGATAACTTTAAGGCTCAGTGGGAATTCGATGTAACTTATCAGAGAATATCTCAAT 1395
DB 541 CGGGATAACTTTAAGGCTCAGTGGGAATTCGATGTAACTTATCAGAGAATATCTCAAT 600
QY 1396 ACAAGATTCCTCAAGTAAATATACAGCAATCTTGATATCTCAACTGAGCTTGGGAATGT 1455
DB 601 ACAAGATTCCTCAAGTAAATATACAGCAATCTTGATATCTCAACTGAGCTTGGGAATGT 660
QY 1456 CAACAACTCGATCAGTAATGCTTTGAATAGTTAGAGGAAGCAACAGAAAACTAGACAA 1515
DB 661 CAACAACTCGATCAGTAATGCTTTGAATAGTTAGAGGAAGCAACAGAAAACTAGACAA 720
QY 1516 AGTCAATGTCAAACTGACATGACATCTGCTCTCACTTACCTATATCGTTTTGACTATCAT 1575
DB 721 AGTCAATGTCAAACTGACATGACATCTGCTCTCATTTACCTATATCGTTTTGACTATCAT 780

QY 1576 ATCTCTTGTGTTTTTGGTATATCTTAGCCTGATTTCTAGCATGCTACCTAATGTACAAGCAAA 1635
DB 781 ATCTCTTGTGTTTTTGGTATATCTTAGCCTGTTCTAGCATGCTACCTAATGTATAAGCAAA 840
QY 1636 GGGCAACAAAAAACCCTTATATGCTTGGGAATAATATCTTAGATCAGATGAGAGCCAC 1695
DB 841 GGGCAACAAAAAGACCTTATATGCTTGGGAATAATATACCTAGATCAGATGAGAGCCAC 900
QY 1696 TACAAAAATGTGAACACACATGAGGAACGAAGTTCCTCAATAGTAATTTGTGTGAAAG 1755
DB 901 TACAAAAATGTGAACACACATGAGGAACGAAGTATCCNAATAGTAATTTGTGNGAAG 960
QY 1756 TTCTGTAGTCTGTCTCAGTTTCAGAGAGTTAAGAAAAAACTACCGGTTGTAGATGACCAAG 1815
DB 961 TTCTGTAGTCTGTCTCAATTCGGAGAGTTTAGAAAAAACTACGCGTTGTAGATGACCAAG 1020
QY 1816 GACGATATACGGGTAGAACGGTAAGAGAGCGCGCCCTCAATTCGAGCCAGCCTTCACA 1875
DB 1021 GACGATATACGGGTAGAACGGTAAGAGAGCGCGCCCTCAATTCGAGCCGGGCTTCACA 1080
QY 1876 ACCTCGTTCTACCGCTTCACCGACAAACAGTCTCTCAATCATGGACCGCGCGTTAGCCAA 1935
DB 1081 ACCTCGTTCTACCGCTTCACCGACAGCAGTCTCTCAGTCATGGACCGCGCAGTTAGCCAA 1140
QY 1936 GTTTCGTTAGAGAAATGATGAAAAGAGAGGCAAAAAATACATGGCGCTTGATATTCGGGATT 1995
DB 1141 GTTTCGTTAGAGAAATGATGAAAAGAGAGGCAAAAAATACATGGCGCTTGATATTCGGGATT 1200
QY 1996 GCAATCTTATTTTAAACAGTAGTAGCCTTGGGCTATATCTGTAGCCTCCCTTTTATATAGC 2055
DB 1201 GCAATCTTATCTTAAACAGTAGTAGCCTTGGGCTATATCTGTAGCCTCCCTTTGTATATAGC 1260
QY 2056 ATGGGGGCTAGCACACCTAGCGATCTTGTAGGCATACCGACTAGGATTTCCAGGGCAGAA 2115
DB 1261 ATGGGGGCTAGCACACCTAGCGATCTTGTAGGCATACCGACAGGATTTCTAGGGCAGAA 1320
QY 2116 GAAAAGATTACATCTACACTTGGTTTCCAATCAAGATGTAGTAGTAGGATATATAAGCAA 2175
DB 1321 GAAAAGATTACATCTGCACTTGGTTTCCAATCAAGATGTAGTAGTAGGATATATAAGCAA 1380
QY 2176 GTGGCCCTTGAGTCTCCGTTGGCATTTGTAATACCTAGAGACCAACAATTAAGACGAATA 2235
DB 1381 GTGGCCCTTGAGTCTCCGTTGGCATTTGTAATACCTAGAGACCAACAATTAAGACGAATA 1440
QY 2236 ACATCTCTCTTATCAGATTAATGAGCTGCAAAACAACAGTGGGTGGGGGACCCCTATC 2295
DB 1441 ACATCTCTCTTATCAGATTAATGAGCTGCAAAACAACAGCGGGTGGGGGACCCCTATC 1500
QY 2296 CATGACCCAGATTTATATAGGGGGATAGGCAAGAACTCATTTGTAGATGATGCTAGTGAT 2355
DB 1501 CATGACCCAGATTTATATCGGGGGATAGGCAAGAACTCATTTGTAGATGATGCTAGTGAT 1560
QY 2356 GTCACATCATTTATCCCTCTGCAATTTCAAGAAACATCTGAAATTTTATCCGGGGCCCTACT 2415
DB 1561 GTCACATCATTTATCCCTCTGCAATTTCAAGAAACATCTGAAATTTTATCCGGGGCCCTACT 1620
QY 2416 ACAGGATCAGGTTGCATCTCGAATACCTCATTTGACATGAGTGTACCATCTACTCTCTAC 2475
DB 1621 ACAGGATCAGGTTGCATCTCGAATACCTCATTTGACATGAGTGTACCATCTACTCTCTAC 1680
QY 2476 ACCATAATGTAAATTTGTCTGGATGCAGATCAGTCACTCATTTATCATATCAGTATTTAGCA 2535
DB 1681 ACTCATAAATGTAAATTTGTCTGGATGCAGATCACTCACTCATCATCAGTATTTAGCA 1740
QY 2536 CTTTGTGTCTCCGGACATCTGCAACAGAGAGGATATTTCTTTTCTACTCTGCGGTTCCATC 2595
DB 1741 CTTTGTGTGTCTCCGGACATCTGCAACAGAGAGGATATTTCTTTTCTACTCTGCGGTTCCATC 1800
QY 2596 AACCTGGACGACACCCAAATCGGAAGTCTTCAGTGTGAGTGCAACTCCCTCGGGTTGT 2655
DB 1801 AGTCTGGATGACACCCAAATCGGAAGTCTTCAGTGTGAGTGCAACTCCCTTAGGTTGT 1860

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Qy 2656 GATATGCTGTCTCGAAAGTCACGGACACAGAGAAAGATTATTAATCACTGAGCTGTCCCT 2715
Db 1861 GATATGCTGTCTCGAAAGTCACGGACACAGAGAAAGATTATTAATCACTGAGCTGTCCCT 1920
Qy 2716 ACGCCGATGTACATGGAGGTTAGGTTTCAGCGCCAGTACACAGAAAGAGACCTAGAT 2775
Db 1921 ACGCTGATGACATGGAGGTTAGGTTTCAGCGCCAGTACACAGAAAGAGACCTAGAC 1980
Qy 2776 GTCAACAATATTTCGGGACTGGGTGGCCAACTACCCAGGAGTGGGGTGGATCTTTT 2835
Db 1981 GTCAACAATATTTCGGGACTGGGTGGCCAACTACCCAGGAGTGGGGTGGATCTTTT 2040
Qy 2836 ATTGACAGCCGCTATGTTCTAGTCTACGGAGGTTAAACCCCAATTCACCCAGTGAC 2895
Db 2041 ATTGACAGCCGCTATGTTCTAGTCTACGGAGGCTGAACCCCAATTCACCCAGTGAC 2100
Qy 2896 ACTGTACAGGAAGGAATATGTATATACAGGATACATGACATGACATGCCAGATGAG 2955
Db 2101 ACTGTACAGGAAGGAATATGTATATACAGGATACATGACATGACATGCCAGATGAG 2160
Qy 2956 CAAGACTACAGATTCCGAATGGCCAACTCTTCGTATTAAGCCTTGGACGGTTTGGTGAAA 3015
Db 2161 CAAGACTACAGATCCGAATGGCCAACTCTTCGTATTAAGCCTTGGTGAAA 2220
Qy 3016 CGCATACAGAGGCTATCTTATCTATCAAGTGTCAACATCCTTAGCGGAAGACCCGGTA 3075
Db 2221 CGCATACAGAGGCTATCTTATCTATCAAGTGTCAACATCCTTTGGCGAAGACCCAGTA 2280
Qy 3076 CTGACTGTACCGCCCAACACAGTCAACACTCATGGGGCCGAAGGCGAATTTCTCACAGTA 3135
Db 2281 CTGACTGTACCGCCCAACACAGTCAACACTCATGGGGCCGAAGGCGAATTTCTCACAGTA 2340
Qy 3136 GGGACATCTCATTTCTTGTATCAACGAGGCTCATCATCTCTCCCGGTTATTATAT 3195
Db 2341 GGGACATCTCATTTCTTGTATCAACGAGGCTCATCATCTCTCCCGGTTATTATAT 2400
Qy 3196 CCTATGACAGTCAGCAACAAACAGCCACTCTTCATAGTCTTATATCAATTCAGCTTC 3255
Db 2401 CCTATGACAGTCAGCAACAAACAGCCACTCTTCATAGTCTTATATCAATTCAGCTTC 2460
Qy 3256 ACTCGGCAGGTAGTATCCCTTGCAGGCTTCAGCAAGATGCCCACTCGTGTTACT 3315
Db 2461 ACTCGGCAGGTAGTATCCCTTGCAGGCTTCAGCAAGATGCCCACTCGTGTTACT 2520
Qy 3316 GGAGTCTATACAGATCCATATCCCTTAATCTTCTATAGAAACC 3358
Db 2521 GGAGTCTATACAGATCCATATCCCTTAATCTTCTATAGGAACC 2563
```

RESULT 8

AAQ68943

ID AAQ68943 standard; DNA; 4177 BP.

XX AC AAQ68943;

XX XX

DT 25-MAR-2003 (revised)

DT 13-APR-1995 (first entry)

XX XX

DE SfII fragment contg. Newcastle Disease Virus HN and F genes.

XX XX

KW SfII fragment; Newcastle Disease Virus; HN gene; F gene; ss.

XX XX

OS Synthetic.

XX XX

FH Key

CDS Location/Qualifiers

FT 115..1860

FT /*tag= a

FT /label= AAR58859

CDS 2095..3756

FT /*tag= b

FT /label= AAR58858

XX XX

PN WO9419014-A1.

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01-SEP-1994.

28-FEB-1994; 94WO-US001826.

26-FEB-1993; 93US-00024156.

(SYTR) SYNTRO CORP.

(JAPG) NIPPON ZEON KK.

Cochran MD;

WPI; 1994-294007/36.

P-PSDB; AAR58858, AAR58859.

New recombinant fowl pox virus for use in vaccines - contains genes

expressing antigens of Newcastle disease virus and opt. infectious

bronchitis virus.

Disclosure; Page 63-68; 85pp; English.

Newcastle Disease Virus (NDV) HN and F genes were inserted as a SfII

fragment into the homology vector 443-88.8 at the unique SfII site. The

NDV HN and F genes were inserted in the same transcriptional orientation

as the ORF in the parental homology vector. The sequence of SfII fragment

is in AAQ68943/AA58858/AA58859. The inserted SfII fragment has the

following structure: Junction A - Fragment 1 (HN, AAs 2-577) - Junction B

- Fragment 2 (F, AAs 1-553) - Junction C - Fragment 3 (pBR322) - Junction

D. Fragment 1 is approx. 1811 bp. Fragment 2 is an approx 1812 bp BamHI to PetI

cDNA clone (B1 strain). Fragment 3 is an approx 1812 bp BamHI to PetI

fragment of the full length NDV F cDNA (B1 Strain). Fragment 3 is an

approx 235 bp PetI and ScaI fragment of the plasmid pBR322. The sequences

of the Junctions are in AAQ68945, AAQ68946, AAQ68947 and AAQ68948.

(Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 4177 BP; 1199 A; 980 C; 910 G; 1088 T; 0 U; 0 Other;

Query Match 51.9%; Score 1741.8; DB 2; Length 4177;

Best Local Similarity 98.8%; Pred. No. 0;

Matches 1755; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

16 TGCATCCCGTTCGGCCCTCCAGGTGCAAGATGGGCTCCAGACCTTCTACCAAGAACCC 75

2064 TCCATCCCGTTCGGCCCTCCAGGTGCAAGATGGGCTCCAGACCTTCTACCAAGAACCC 2123

76 AGCACCTATGATGCTGACTATCGGGTTCGGCTGGCACTGAGTTGCACTGTCCGCAAA 135

2124 AGCACTATGATGCTGACTATCGGGTTCGGCTGGCACTGAGTTGCACTGTCCGCAAA 2183

136 CTCATTGATGGCAGGCTCTTGCAGCTGCAGGAATTGTTGTTACAGGAGACAAAGCGT 195

2184 CTCATTGATGGCAGGCTCTTGCAGCTGCAGGAATTGTTGTTACAGGAGACAAAGCGT 2243

196 CACATATACACCTCATCCAGACAGGATCAATCATAGTTAAGCTCTCCCGAATCTGCC 255

2244 CACATATACACCTCATCCAGACAGGATCAATCATAGTTAAGCTCTCCCGAATCTGCC 2303

256 CAAGGATAAGGAGGATGTGCGAAAGCCCTTGGATGCATACAAAGGACATTGACAC 315

2304 AAGGATAAGGAGGATGTGCGAAAGCCCTTGGATGCATACAAAGGACATTGACAC 2363

316 TTTGCTCACCCCTTTGGTGAATCTATCCGTAGGATACAAAGAGTCTGTGACTACATCTGG 375

2364 TTTGCTCACCCCTTTGGTGAATCTATCCGTAGGATACAAAGAGTCTGTGACTACATCTGG 2423

376 AGGGGGAGACAGGGGGCTTATAGCGCATATTGGCGGTGTGGCTCTTGGGGTGC 435

2424 AGGGGGAGACAGGGGGCTTATAGCGCATATTGGCGGTGTGGCTCTTGGGGTGC 2483

436 AACTGCCGCAAAATAACACGCGCGAGCTCTGATACAAAGCCAAACAAATGCTGCAA 495

2484 AACTGCCGCAAAATAACACGCGCGAGCTCTGATACAAAGCCAAACAAATGCTGCAA 2543

496 CATCTCTCCGACTTAAAGAGAGCATTTGCCGCAACCAATGAGGCTGTGCATGAGTCACTGA 555
Db
2544 CATCTCCGACTTAAAGAGAGCATTTGCCGCAACCAATGAGGCTGTGCATGAGTCACTGA 2603
Qy 556 CGGATTATCGCAACTAGCAGTGGCAGTTGGGAAGATGCGACAGTTTGTAAATGACCAATT 615
Db 2604 CGGATTATCGCAACTAGCAGTGGCAGTTGGGAAGATGCGACAGTTTGTAAATGACCAATT 2663
Qy 616 TATATAAACAGCTTCAGGAATTAGACTGCATCAAAATTTGCACCAAGTTGGTGTAGAGCT 675
Db 2664 TATATAAACAGCTTCAGGAATTAGACTGCATCAAAATTTGCACCAAGTTGGTGTAGAGCT 2723
Qy 676 CAACCTGTACTAACCGAATTGACTACAGTATTTCGGAACCAAAATCACTTCACCTGCTTT 735
Db 2724 CAACCTGTACTAACCGAATCGACTACAGTATTTCGGAACCAAAATCACTTCACCTGCCIT 2783
Qy 736 AAACAAGCTGACTATTTCAGGCACTTTTACAATCTAGCTGGTGGAAATATGGAATTACTTATT 795
Db 2784 AAACAAGCTGACTATTTCAGGCACTTTTACAATCTAGCTGGTGGAAATATGGAATTACTTATT 2843
Qy 796 GACTAAGTTAGGTAGGGAACCAATCAACTCAGCTCAATTAATCGGTAGCGGCTTATCAC 855
Db 2844 GACTAAGTTAGGTATAGGGAACCAATCAACTCAGCTCAATTAATCGGTAGCGGCTTATCAC 2903
Qy 856 CGGTAAACCTTATTTCTATACGACTCACAGACTCAACTCTTGGGTATACAGGTAACCTTACC 915
Db 2904 CGGTAAACCTTATTTCTATACGACTCACAGACTCAACTCTTGGGTATACAGGTAACCTTACC 2963
Qy 916 TTCAGTGGGAACCTTAAATTAATATGGGTGCCA CTTACTTGGAAACCTTATTCGTTAAGCAC 975
Db 2964 TTCAGTGGGAACCTTAAATTAATATGGGTGCCA CTTACTTGGAAACCTTATTCGTTAAGCAC 3023
Qy 976 AACCGGGATTTGGCTCGGCACTTGTCCCAAGTGGTGACACAGTGGTTCGTGAT 1035
Db 3024 AACCGGGATTTGGCTCGGCACTTGTCCCAAGTGGTGACACAGTGGTTCGTGAT 3083
Qy 1036 AGAAGAACTTGACACCTCATPACTGTATAGAACTGACTTATATATTTGTACAAGAAAT 1095
Db 3084 AGAAGAACTTGACACCTCATPACTGTATAGAACTGACTTATATATTTGTACAAGAAAT 3143
Qy 1096 AGTAAAGTTCCCTATGTCCTCGGTATTTATTCCTGTTGAGCGGCAATACGTCGGCCTG 1155
Db 3144 AGTAAAGTTCCCTATGTCCTCGGTATTTATTCCTGTTGAGCGGCAATACGTCGGCCTG 3203
Qy 1156 TATGTACTCAAGACCGAGCGGCACCTTACTACACCATACATCACTATCAAAAGGTTCACT 1215
Db 3204 TATGTACTCAAGACCGAGCGGCACCTTACTACACCATACATCACTATCAAAAGGTTCACT 3263
Qy 1216 CATCGCCAACTGCAAGATGACAACATGTAGATGTGTAACCCCGGGTATCATATCGCA 1275
Db 3264 CATCGCTTACTGCAAGATGACAACATGTAGATGTGTAACCCCGGGTATCATATCGCA 3323
Qy 1276 AAATATGGAAGACCGGTGCTCTAATAGATAAACAATCATGCAATGTTTTATCCTTAGG 1335
Db 3324 AAATATGGAAGACCGGTGCTCTAATAGATAAACAATCATGCAATGTTTTATCCTTAGG 3383
Qy 1336 CGGGATAACTTTAAGCTCAGTGGGNAATTCGATGTAACTTATCAGAGATATCTCAAT 1395
Db 3384 CGGGATAACTTTAAGCTCAGTGGGNAATTCGATGTAACTTATCAGAGATATCTCAAT 3443
Qy 1396 ACAAGATTCCTCAAGTATAATAACAGGCAATCTTGATATCTCAACTGAGCTGGGAATGT 1455
Db 3444 ACAAGATTCCTCAAGTATAATAACAGGCAATCTTGATATCTCAACTGAGCTGGGAATGT 3503
Qy 1456 CAACAACCTGATCAGTAATGCTTTGAATAAGTTAGAGGAAGCAACAGAAAACTAGACAA 1515
Db 3504 CAACAACCTGATCAGTAATGCTTTGAATAAGTTAGAGGAAGCAACAGAAAACTAGACAA 3563
Qy 1516 AGTCAATGTCAAACTGATGACACACTGCTCTCAATACCTATATCGTTTTGACTATCAT 1575
Db 3564 AGTCAATGTCAAACTGATGACACACACTGCTCTCAATACCTATATCGTTTTGACTATCAT 3623
Qy 1576 ATCTCTTTGTTTGGTATACTTAGCCTGATTCTAGCATGCTACCTAATGTACAAGCAAAA 1635

Db 3624 ATCTCTGTTTGGTATACTTAGCTGATTCTAGCATGCTACCTAATGTACAAGCAAAA 3683
Qy 1636 GGGCAACAAAAACCTTATTATGCTTGGGAATATATCTTAGATCAGATGAGAGCCAC 1695
Db 3684 GGGCAACAAAAAGACCTTATTATGCTTGGGAATATATCCTTAGATCAGATGAGAGCCAC 3743
Qy 1696 TACAAAAATGTGAACACAGATGAGGAACGAAGTTTCCCTTAATAGTAATTTGTGTGAAG 1755
Db 3744 TACAAAAATGTGAACACAGATGAGGAACGAAGTTTCCCTTAATAGTAATTTGTGTGAAG 3803
Qy 1756 TTCTGTAGTCTGTCTAGTTTCAGAGATTAGAAAAA 1792
Db 3804 TTCTGTAGTCTGTCTAGTTTCGAGAGTTAAGAAAAA 3840
RESULT 9
AAQ70570
ID AAQ70570 standard; DNA; 4177 BP.
XX AAQ70570;
AC AAQ70570;
XX 25-MAR-2003 (revised)
DT 14-APR-1995 (first entry)
XX
XX Sfil fragment contg. Newcastle disease virus HN and F genes.
XX Newcastle disease virus; HN gene; F gene; Sfil; vector 502-26.22; ss.
XX Synthetic.
FH Location/Qualifiers
FT 115..1860
CDS /*tag= a
FT /*label= AARS8598, HN
FT 2095..3756
CDS /*tag= b
FT /*label= AAR49141, F
XX
PN WO9419015-A1.
XX
XX 01-SEP-1994.
PD
XX 28-FEB-1994; 94WO-US002252.
PF
XX 26-FEB-1993; 93US-00024156.
PR
XX (SYTR) SYNTRO CORP.
PA
XX Cochran MD;
PI
XX WPI; 1994-294008/36.
DR P-PSDB; AARS8598, AAR49141.
XX
XX New recombinant fowl pox viruses - useful as vaccines against fowl pox virus, Newcastle Disease Virus and infectious laryngotracheitis virus.
PT
XX Disclosure; Page 72-77; 97pp; English.
PS
XX AAQ70570 is the Sfil fragment insert in Homology Vector 502-26.22 contg. Newcastle disease virus (NDV) HN and F genes. The structure of the fragment is: 5'- Junction A - Fragment 1 (NDV HN AAs 2-577) - Junction B - Fragment 2 (NDV P AAs 1-553) - Junction C - Fragment 3 (pBR322) - Junction D - 3'. Fragment 1 is Avail to NaeI fragment of the full length NDV HN cDNA clone (BI strain). Fragment 2 is BamHI to PstI fragment of the full length NDV F cDNA (BI strain). Fragment 3 is a PstI and ScaI fragment of pBR322. The structures of the Junctions A, B, C and D are given in AAQ70552, AAQ70553, AAQ70554 and AAQ70555 respectively. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 4177 BP; 1199 A; 980 C; 910 G; 1088 T; 0 U; 0 Other;
SQ

Query Match 51.9%; Score 1741.8; DB 2; Length 4177;

Best Local Similarity 98.8%; Pred. No. 0; Matches 1755; Conservative 0; Mismatches 22; Indels 0; Gaps 0;			
Qy	16	TGGATCCCGGTGGCGGCTCCAGGTGCAAGATGGGTCCAGACTCTTCTACCAAGAACCC	75
Db	2064	TCGATCCCGGTGGCGGCTCCAGGTGCAAGATGGGTCCAGACTCTTCTACCAAGAACCC	2123
Qy	76	AGCACTATGATGCTGACTATCCGGTGGCTGGCACTGAGTTGCAATCTGTCCGCAAA	135
Db	2124	AGCACTATGATGCTGACTATCCGGTGGCTGGCACTGAGTTGCAATCTGTCCGCAAA	2183
Qy	136	CTCCATTGATGGCAGGCTCTTGAGCTGCAAGTAATGCTTACAGAGCAAGCGT	195
Db	2184	CTCCATTGATGGCAGGCTCTTGAGCTGCAAGTAATGCTTACAGAGCAAGCGT	2243
Qy	196	CAACATATACACCTCATCCAGACAGGATCAATATAGTTAAGCTCTCCCGAATCTGCC	255
Db	2244	CAACATATACACCTCATCCAGACAGGATCAATATAGTTAAGCTCTCCCGAATCTGCC	2303
Qy	256	CAAGGATAAGAGGATGTGCGAAGCCCTTGGATGCATACAAACAGGACATTTGACAC	315
Db	2304	AAAGGATAAGAGGATGTGCGAAGCCCTTGGATGCATACAAACAGGACATTTGACAC	2363
Qy	316	TTTGCTCACCCCTTGGTGAATCTATCCGTAGGATACAGAGTCTGTGACTACATCTGG	375
Db	2364	TTTGCTCACCCCTTGGTGAATCTATCCGTAGGATACAGAGTCTGTGACTACATCTGG	2423
Qy	376	AGGGGGAGACAGGGGGCTTATAGCGCCATTTATGGCGGTGGCTCTTGGGGTTGC	435
Db	2424	AGGGGGAGACAGGGGGCTTATAGCGCCATTTATGGCGGTGGCTCTTGGGGTTGC	2483
Qy	436	AACCTGCGCAAAATAACAGCGCGCGAGTCTGATACAAAGCCAAAACAAATGTCGCAA	495
Db	2484	AACCTGCGCAAAATAACAGCGCGCGAGTCTGATACAAAGCCAAAACAAATGTCGCAA	2543
Qy	496	CATCTCGACTTAAGAGACATTTGCGGCAACCAATGAGGCTGTGATGAGTCACTGA	555
Db	2544	CATCTCGACTTAAGAGAGCATTTGCGGCAACCAATGAGGCTGTGATGAGTCACTGA	2603
Qy	556	CGGATATCGCAACTAGCAGTGGCAGTTGGGAAGATGCGAGTGTGTTAATGACCAATT	615
Db	2604	CGGATATCGCAACTAGCAGTGGCAGTTGGGAAGATGCGAGTGTGTTAATGACCAATT	2663
Qy	616	TAATAAACAGCTCAGGAATTAGCTCATCAAAATTCACAGCAAGTTGGTGTAGAGCT	675
Db	2664	TAATAAACAGCTCAGGAATTAGAGTGCATCAAAATTCACAGCAAGTTGGTGTAGAGCT	2723
Qy	676	CAACTGTACTAACCGAATTGACTACAGTATTCGGACCAACATCACTTCACCTGCTTT	735
Db	2724	CAACTGTACTAACCGAATTCGACTACAGTATTCGGACCAACATCACTTCACCTGCTTT	2783
Qy	736	AAACAAGCTGACTATTTCAGGCACCTTACAATCTAGCTGGTGGAAATATGGATTACTTTAT	795
Db	2784	AAACAAGCTGACTATTTCAGGCACCTTACAATCTAGCTGGTGGAAATATGGATTACTTTAT	2843
Qy	796	GACTAAGTTAGGTAGGAGCAACATCAACTCAGCTCAATTAATCGGTAGCGGCTTAATCAC	855
Db	2844	GACTAAGTTAGGTATAGGAAACATCAACTCAGCTCAATTAATCGGTAGCGGCTTAATCAC	2903
Qy	856	CGGTAAACCTTATCTATACGACTCAGACTCACTCTTGGGTATACAGGTAACCTTACC	915
Db	2904	CGGTAAACCTTATCTATACGACTCAGACTCACTCTTGGGTATACAGGTAACCTTACC	2963
Qy	916	TTCACTCGGGAACCTAAATAATATGCGTGGCCACCTACTTGGAAACCTTATCCGTAAGCAC	975
Db	2964	TTCACTCGGGAACCTAAATAATATGCGTGGCCACCTACTTGGAAACCTTATCCGTAAGCAC	3023
Qy	976	AACCAAGGGATTTGCTCGGCATTTGTCGCAAAAGTGGTGCACAGGTCGGTCTGTGAT	1035
Db	3024	AACCAAGGGATTTGCTCGGCATTTGTCGCAAAAGTGGTGCACAGGTCGGTCTGTGAT	3083
Qy	1036	AGAAAGACTTGACACCTACTGATAGAACTGACTTATGATTTATTTGTACAGAAAT	1095

Db	3084	AGBAGAACTTGACACCTCATCTGTATAGAACTGACTTAGATTATTTGTACAGAAT	3143
Qy	1096	AGTAACGTTCCCTATGTCCTGATTTTATTCCTGCTGAGCGGCAATACGTCGGCTG	1155
Db	3144	AGTAACGTTCCCTATGTCCTGATTTTATTCCTGCTGAGCGGCAATACATCGGCTG	3203
Qy	1156	TATGTACTCAAGACCGAAGCGCACTTACTACACCATACATGACTCAAGGTTCAAGT	1215
Db	3204	TATGTACTCAAGACCGAAGCGCACTTACTACACCATATATGACTATCAAGGCTCAGT	3263
Qy	1216	CATCGCAACTGCAAGATGACCAATGTAGATGTGTAACCCCGGGTATCATATCGCA	1275
Db	3264	CATCGCTAATGCAAGATGACCAATGTAGATGTGTAACCCCGGGTATCATATCGCA	3323
Qy	1276	AAACTATGGAAGCCGCTGTCTTAATAGATAAACAATCATGCAATGTTTATCCTTAGG	1335
Db	3324	AAACTATGGAAGCCGCTGTCTTAATAGATAAACAATCATGCAATGTTTATCCTTAGG	3383
Qy	1336	CGGGATTAACCTTAAGGCTCAGTGGGAAATTCGATGTAACCTTATCAGAGATATCTCAAT	1395
Db	3384	CGGGATTAACCTTAAGGCTCAGTGGGAAATTCGATGTAACCTTATCAGAGATATCTCAAT	3443
Qy	1396	ACAAGATTCTCAAGTAATAAACAAGCAATCTTGATATCTCAACTGAGCTTGGGAATGT	1455
Db	3444	ACAAGATTCTCAAGTAATAAACAAGCAATCTTGATATCTCAACTGAGCTTGGGAATGT	3503
Qy	1456	CAACAACCTCGATCAGTAATGCTTTGAATAAGTTAGAGGAAGCAACAGAAAACCTAGACAA	1515
Db	3504	CAACAACCTCGATCAGTAATGCTTTGAATAAGTTAGAGGAAGCAACAGAAAACCTAGACAA	3563
Qy	1516	AGTCAATGTCAAACTGACTAGCACATCTGCTCATTTACCTATATCTGTTTGTACTATCAT	1575
Db	3564	AGTCAATGTCAAACTGACTAGCACATCTGCTCATTTACCTATATCTGTTTGTACTATCAT	3623
Qy	1576	ATCTCTTGTGTTTGGTATCTTAGCCTGATTCTAGCATGCTACCTAATGTACAGCAAAA	1635
Db	3624	ATCTCTTGTGTTTGGTATCTTAGCCTGATTCTAGCATGCTACCTAATGTACAGCAAAA	3683
Qy	1636	GGCGCAACAAAAACCTTATTATGGCTTGGGAATAATACCTAGATCAGATGAGAGCCAC	1695
Db	3684	GGCGCAACAAAAACCTTATTATGGCTTGGGAATAATACCTAGATCAGATGAGAGCCAC	3743
Qy	1696	TACAAAAATGTGAACACAGATGAGGAACGAAGGTTTCCCTAATAGTAATTTGTGTGAAG	1755
Db	3744	TACAAAAATGTGAACACAGATGAGGAACGAAGGTTTCCCTAATAGTAATTTGTGTGAAG	3803
Qy	1756	TTCTGTGTAGTCTGTGCTCAGAGAGTTAAGAAAAA 1792	
Db	3804	TTCTGTGTAGTCTGTGCTCAGAGAGTTAAGAAAAA 3840	
RESULT 10			
AAT48510			
ID	AAT48510 standard; DNA; 4177 BP.		
XX	AAT48510;		
XX	AC AC		
DT	05-MAY-1997 (first entry)		
XX	SfiI fragment encoding Newcastle disease virus HN and F genes.		
DE	Fowlpox virus; FPV; recombinant virus; vector; vaccine; immunisation;		
KW	Newcastle disease virus; NDV; haemagglutinin; fusion protein; poultry;		
KW	ds.		
XX	Newcastle disease virus.		
OS			
XX	Key Location/Qualifiers		
PH	115..1860		
FT	/*tag= a		
FT	/product= "NDV haemagglutinin"		
FT	2095..3756		
FT	/*tag= b		

FT	/product= "NDV fusion protein"
XX	WO9640880-A1.
XX	PN
XX	PD
XX	19-DEC-1996.
XX	
XX	04-JUN-1996; 96WO-US011187.
PF	
XX	07-JUN-1995; 95US-00484790.
XX	
XX	(SVTR) SYNTRO CORP.
PA	
PI	Cochran MD, Junker DE, Singer PA;
XX	
XX	WPI; 1997-087060/08.
DR	P-PSDB; AAW10690, AAW10691.
DR	
XX	
XX	New recombinant fowlpox virus - contg. a foreign DNA sequence inserted
PT	into the fowlpox virus genome, used for the prodn. of vaccines.
XX	
XX	Disclosure; Page 102-107; 134pp; English.
PS	
XX	
CC	An SfII fragment (AAAT48510), contg. coding sequences for Newcastle
CC	disease virus (NDV) haemagglutinin (HN) (AAWI0690) and fusion protein (F)
CC	(AAWI0691), was inserted into homology vector 443-88.8 (see also
CC	AAAT48511) at the unique SfiII site, yielding homology vector 502-26.22
CC	(see also AAAT48502-05). The NDV HN and F genes were inserted in the same
CC	transcriptional orientation as the parental homology vector. 502-26.22
CC	was used to insert the NDV HN and F genes into fowlpox virus. The
CC	resulting recombinant virus can be used to deliver the vaccine antigens
CC	to poultry
XX	
SQ	Sequence 4177 BP; 1199 A; 980 C; 910 G; 1088 T; 0 U; 0 Other;
Query Match 51.9%; Score 1741.8; DB 2; Length 4177;	
Best Local Similarity 98.8%; Pred. No. 0;	
Matches 1755; Conservative 0; Mismatches 22; Indels 0; Gaps 0;	
QY	16 TGGATCCCGTGTGGCGCCTCCAGGTCGAAGATGGCTCCAGACCTTCTACCAAGAACC 75
DB	2064 TCGATCCCGTTGGCGCCTCCAGGTCGAAGATGGCTCCAGACCTTCTACCAAGAACC 2123
QY	76 AGCACCTATGATCTGACTATCCGGTTCGCCTGGCAGCTGATGTCATCTCTGCCGCAA 135
DB	2124 AGCACCTATGATCTGACTATCCGGTTCGCCTGGTACTGATGTCATCTCTGCCGCAA 2183
QY	136 CTCATTATGGCAGGCCCTTCGAGCTCCAGGAATTTGGTTTACAGAGACAAGCGGT 195
DB	2184 CTCATTATGGCAGGCCCTTCGAGCTCCAGGAATTTGGTTTACAGAGACAAGCGGT 2243
QY	196 CAACATATACCTCATCCAGACAGGATCAATCATAGTTAAGCTCCCTCCGATCTGCC 255
DB	2244 CAACATATACCTCATCCAGACAGGATCAATCATAGTTAAGCTCCCTCCGATCTGCC 2303
QY	256 CAAGGATAAGGAGGCATGTGCGAAGACCCCCTTGATGCGATACAAAGGACATTCAC 315
DB	2304 ABAGGATAAGGAGGCATGTGCGAAGACCCCCTTGATGCGATACAAAGGACATTCAC 2363
QY	316 TTGTGCTACCCCCCTTGGTGACTCTATCCGTAAGGATACAAAGTCTGTGACTACATCTGG 375
DB	2364 TTGTGCTACCCCCCTTGGTGACTCTATCCGTAAGGATACAAAGTCTGTGACTACATCTGG 2423
QY	376 AGGGGGAGACAGGGGGCCTTATAGGCGCCATTTAGCGGTGGCGCTTTGGGGTTGC 435
DB	2424 AGGGGGAGACAGGGGGCCTTATAGGCGCCATTTAGCGGTGGCGCTTTGGGGTTGC 2483
QY	436 AACTGCGCACAAATAACAGCGCGCCAGCTCTGATACAAAGCCAAACAAAATGTCGCCAA 495
DB	2484 AACTGCGCACAAATAACAGCGCGCCAGCTCTGATACAAAGCCAAACAAAATGTCGCCAA 2543
QY	496 CATCTCCGACTTAAAGAGAGCATTTCCGCCAACCAATGAGGCTGTGCATGAGGTCATGA 555
DB	2544 CATCTCCGACTTAAAGAGAGCATTTCCGCCAACCAATGAGGCTGTGCATGAGGTCATGA 2603

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Qy 1636 GGCGCAACAAAACCTTATTATGGCTTGGGAATATACCTAGATCATGATGAGCCAC 1695
Db 3684 GGCGCAACAAAAGACCTTATTATGGCTTGGGAATATATACCTAGATCAGATGAGCCAC 3743
Qy 1696 TACAATAATGTGAACACAGATGAGGAACGAAGTTTCCCTAAATAGTAATTTGTGTAAG 1755
Db 3744 TACAATAATGTGAACACAGATGAGGAACGAAGTTTCCCTAAATAGTAATTTGTGTAAG 3803
Qy 1756 TTCTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1792
Db 3804 TTCTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3840

RESULT 11
AAx81147
ID AAx81147 standard; DNA; 4177 BP.
XX
XX
AC AAx81147;
XX
XX 07-SEP-1999 (first entry)
XX
XX Seq ID No: 12 of US925358.
XX
XX Fowlpox virus; FPV; recombinant; vaccine; immunisation; chicken; NDV;
XX Newcastle disease virus; NDV; Fowlpox; Infectious Laryngotracheitis; ds.
XX
XX Fowlpox virus.
XX
XX Key Location/Qualifiers
XX CDS 115..1860
XX FT /*tag= a
XX FT 2095..3756
XX FT /*tag= b
XX
XX US925358-A.
XX
XX 20-JUL-1999.
XX
XX 07-JUN-1995; 95US-00484575.
XX
XX 26-FEB-1993; 93US-00024156.
XX 28-FEB-1994; 94WO-US002252.
XX
XX (SYTR ) SYNTRO CORP.
XX
XX Junker DE, Cochran MD;
XX
XX WPI; 1999-418249/35.
XX P-PSDB; AAY21982, AAY21983.
XX
XX Fowlpox viruses, useful as vaccines for immunization of chickens/turkeys
XX against Fowlpox and Newcastle disease virus.
XX
XX Disclosure; Col 61-70; 108pp; English.
XX
XX The invention relates to a recombinant fowlpox virus (FPV) comprising a
XX foreign DNA inserted into a region of the fowlpox virus genome
XX corresponding to a 2.8 kb EcoRI fragment, capable of being expressed in a
XX host cell. The virus is used as a vaccine for immunising chickens against
XX Newcastle disease virus (NDV), Fowlpox, and Infectious Laryngotracheitis
XX
XX Sequence 4177 BP; 1199 A; 980 C; 910 G; 1088 T; 0 U; 0 Other;

Query Match 51.98; Score 1741.8; DB 2; Length 4177;
Best Local Similarity 98.8; Pred. No. 0;
Matches 1755; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

Qy 16 TGGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACCTTCTTACCAAGAACCC 75
Db 2064 TCGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACCTTCTTACCAAGAACCC 2123
Qy 76 AGCACTATGATGCTGACTATCCGGGTTGGCGCTGGCACTGAGTTGCAATCTGTCCGCAAA 135
Db 135
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Db 2124 AGCACTATGATGCTGACTATCCGGGTGGCGCTGGTACTGAGTTGCATCTGTCCGCAAA 2183
Qy 136 CTCATTGTATGGCAGCCCTCTTGCAGCTGCAGAAATTTGTGTTTACAGGAGACAAAGCCGT 195
Db 2184 CTCATTGTATGGCAGCCCTCTTGCAGCTGCAGAAATTTGTGTTTACAGGAGACAAAGCAGT 2243
Qy 196 CACATATACCTCATCCAGACAGGATCAATCATAGTTAAAGCTCTCTCCCGAATCTGCC 255
Db 2244 CAAATATACCTCATCCAGACAGGATCAATCATAGTTAAAGCTCTCTCCCGAATCTGCC 2303
Qy 256 CAAAGATTAAGGAGGCGATGTGCGAAAGCCCTTGGATGCATACAAACAGGACATTTGACCAC 315
Db 2304 AAAGATTAAGGAGGCGATGTGCGAAAGCCCTTGGATGCATACAAACAGGACATTTGACCAC 2363
Qy 316 TTTGCTCACCCCTTTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 375
Db 2364 TTTGCTCACCCCTTTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2423
Qy 376 AGGGGGGAGACAGGGGGCGCTTATAGCGGCATTTATGGCGCTTATGGCGGTGTGGGTGTGC 435
Db 2424 AGGGGGGAGACAGGGGGCGCTTATAGCGGCATTTATGGCGGTGTGGGTGTGTGGGTGTGC 2483
Qy 436 AACTGCGGCACAAATAACAGCGCGCGCAGCTCTGTATACAGCCAAACAAATCTGTGCCAA 495
Db 2484 AACTGCGGCACAAATAACAGCGCGCGCAGCTCTGTATACAGCCAAACAAATCTGTGCCAA 2543
Qy 496 CATCTCCGACTTAAAGAGAGACAATTGCCCAACCAATGAGGCTGTGCATGAGTCACTGA 555
Db 2544 CATCTCCGACTTAAAGAGAGACAATTGCCCAACCAATGAGGCTGTGCATGAGTCACTGA 2603
Qy 556 CGGATTAATGCAACTAGTAGTGTGCGAGTTGGGAAGATGCAGCAGTTTGTATGACCAATTT 615
Db 2604 CGGATTAATGCAACTAGTAGTGTGCGAGTTGGGAAGATGCAGCAGTTTGTATGACCAATTT 2663
Qy 616 TAATAAAACAGCTCAGCAATTTAGACTGTCATCAAAAATTTGCACAGCAAGTTGTTGTAGAGCT 675
Db 2664 TAATAAAACAGCTCAGCAATTTAGACTGTCATCAAAAATTTGCACAGCAAGTTGTTGTAGAGCT 2723
Qy 676 CAACTGTACTAACCGAATTTGACTAGTATTCGGAACCAAAATCACTTCACTTCACTGCTTT 735
Db 2724 CAACTGTACTAACCGAATTTGACTAGTATTCGGAACCAAAATCACTTCACTTCACTGCTTT 2783
Qy 736 AAACAAGCTGACTATTTCAGCAGCTTTACATCTAGCTGTGGTGGAAATATGATTAATTTATT 795
Db 2784 AAACAAGCTGACTATTTCAGCAGCTTTACATCTAGCTGTGGTGGAAATATGATTAATTTATT 2843
Qy 796 GACTAAGTTAGGTAGGGAACCAATCAACTCAGCTCAATTAATCGGTAGCGGCTTAATCAC 855
Db 2844 GACTAAGTTAGGTATAGGGAACCAATCAACTCAGCTCAATTAATCGGTAGCGGCTTAATCAC 2903
Qy 856 CGGTAACCCCTATTCTATACGACTCAGACTCAACTCTTGGGTATACAGGTAACCTTACC 915
Db 2904 CGGTAACCCCTATTCTATACGACTCAGACTCAACTCTTGGGTATACAGGTAACCTTACC 2963
Qy 916 TTCAGTGGGAACTAAATAATATGCTGTCCTTCTTGGAAACCTTATCCGTAAGCAC 975
Db 2964 TTCAGTGGGAACTAAATAATATGCTGTCCTTCTTGGAAACCTTATCCGTAAGCAC 3023
Qy 976 AACGAGGGATTTGCTCGGCACTTGTCCCAAGGTGTCACAGGTCGGTTCCTGTGAT 1035
Db 3024 AACGAGGGATTTGCTCGGCACTTGTCCCAAGGTGTCACAGGTCGGTTCCTGTGAT 3083
Qy 1036 AGAAGAACTTGACACCTCATCTGTATAGAACTGACTTAGATTTATTTGTACAAGAAAT 1095
Db 3084 AGAAGAACTTGACACCTCATCTGTATAGAACTGACTTAGATTTATTTGTACAAGAAAT 3143
Qy 1096 AGTAAGCTTCCCTATGTCCCTCGTATTTATCTGCTTGGCGGCAATAGCTCGGCTG 1155
Db 3144 AGTAAGCTTCCCTATGTCCCTCGTATTTACTCTGCTTGGCGGCAATAGCTCGGCTG 3203
Qy 1156 TATGTACTCAAGACCGAAGCGCACTTACTACACCATACATGACTATCAAGGTTTCAGT 1215
Db 3204 TATGTACTCAAGACCGAAGCGCACTTACTACACCATATATGACTATCAAGGTTTCAGT 3263
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QY 1216 CATCGCCAACTGCAAGATGACAAATGTAGATGTATAACCCCGGGTATCATATCGCA 1275
DB |||||
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QY 1276 AAACATATGGAGAACCGGTGTCTTAATAGATAAACAATCATGCAATGTTTTATCCTTAGG 1335
DB |||||
DB 3324 AAACATATGGAGAACCGGTGTCTTAATAGATAAACAATCATGCAATGTTTTATCCTTAGG 3383
QY 1336 CGGGATAAATTTAAGGCTAGTGGGAATTCGATGTAACCTTATCAGAGAAATATCTCAAT 1395
DB |||||
DB 3384 CGGGATAAATTTAAGGCTAGTGGGAATTCGATGTAACCTTATCAGAGAAATATCTCAAT 3443
QY 1396 ACAAGATTTCTCAAGTAATAATAACAGCAATCTTGATATCTCAACTGAGCTTGGGAATGT 1455
DB |||||
DB 3444 ACAAGATTTCTCAAGTAATAATAACAGCAATCTTGATATCTCAACTGAGCTTGGGAATGT 3503
QY 1456 CAACAACATCGATAGTAATGCTTTGAATAAGTTAGAGAAAGCAACAGAAAACTAGACAA 1515
DB |||||
DB 3504 CAACAACATCGATAGTAATGCTTTGAATAAGTTAGAGAAAGCAACAGAAAACTAGACAA 3563
QY 1516 AGTCATGTCAAACTGACTAGACATCTGCTCTCATTAACCTATATCGTTTGTACTATCAT 1575
DB |||||
DB 3564 AGTCATGTCAAACTGACTAGACATCTGCTCTCATTAACCTATATCGTTTGTACTATCAT 3623
QY 1576 ATCTCTTGTGTTTGGTATATAGCCCTGATTCTAGCATGCTACCTAATGTACAGCAAAA 1635
DB |||||
DB 3624 ATCTCTTGTGTTTGGTATATAGCCCTGATTCTAGCATGCTACCTAATGTACAGCAAAA 3683
QY 1636 GGCGCAACAAAAACCTTATATATGCTTGGGAATAATATCTTAGATCAGATGAGAGCCAC 1695
DB |||||
DB 3684 GGCGCAACAAAAACCTTATATATGCTTGGGAATAATATACCTAGATCAGATGAGAGCCAC 3743
QY 1696 TACAAAAATGTGAACAGATGAGAACGAGGTTTCCCTAATAGTAATTTGTGTGAAG 1755
DB |||||
DB 3744 TACAAAAATGTGAACAGATGAGAACGAGGTTTCCCTAATAGTAATTTGTGTGAAG 3803
QY 1756 TTCTGTGTAGTCTCTAGTTCAGAGAGTTTAAGAAAAA 1792
DB |||||
DB 3804 TTCTGTGTAGTCTCTAGTTCAGAGAGTTTAAGAAAAA 3840
```

RESULT 12

AAZ49295

ID AAZ49295 standard; cDNA; 4177 BP.

XX AAZ49295;

XX AAZ49295;

DT 14-MAR-2000 (first entry)

XX cDNA encoding NDV haemagglutinin-neuraminidase and fusion proteins.

DE cDNA encoding NDV haemagglutinin-neuraminidase and fusion proteins.

XX Fowlpox virus; FPV; recombinant; antigenic protein; expression;

XX infectious laryngotracheitis virus; ILTV; Newcastle disease virus; NDV;

KW Marek's disease virus; cytokeratin; promoter; homologous recombination;

KW homology vector; multivalent; live vaccine; haemagglutinin;

KW neuraminidase; fusion protein; ds.

XX Newcastle disease virus.

OS Newcastle disease virus.

FH Key

XX Location/Qualifiers

FH 115..1860

CDS

FT /tag= a

FT /product= "Haemagglutinin-neuraminidase (HN, AAY58182)"

FT 2095..3756

FT /tag= b

FT /product= "Fusion (F) protein (AAY58183)"

FT

FT

PN US6001369-A.

XX

XX 14-DEC-1999.

PD

XX

XX 07-JUN-1995;

XX 95US-00477459.

PF

XX 26-FEB-1993; 93US-00024156.

PR 28-FEB-1994; 94WO-US002252.

XX (SYTR) SYNTRO CORP.

PA Junker DE, Cochran MD;

PI WPI; 2000-071638/06.

XX P-PSDB; AAY58182, AAY58183.

DR Recombinant fowlpox virus useful as a vaccine for immunizing fowl against

XX Marek's disease, Newcastle disease, Infectious laryngotracheitis Virus

PT and/or fowlpox.

XX Claim 5; Col 61-68; 56pp; English.

PS The invention relates to a recombinant fowlpox virus (FPV) comprising a

XX foreign DNA inserted into a 4.2 kb EcoRI fragment of the fowlpox virus

CC genome. The foreign DNA is capable of being expressed in a host cell into

CC which the fowlpox virus has been introduced and encodes an antigenic

CC protein. The antigenic protein which may be expressed includes infectious

CC laryngotracheitis virus (ILTV) glycoprotein B (gB) or glycoprotein D (gD,

CC AAY58184), Newcastle disease virus (NDV) haemagglutinin (HN, AAY58182) or

CC fusion (F) protein (AAY58183) and Marek's disease virus gB or gD. The

CC foreign DNA may alternatively encode a cytokine such as chicken

CC myelomonocytic growth factor (CMGF) or cytokine interferon (cIFN). The

CC foreign DNA in the recombinant FPV is under the control of one or more

CC synthetic pox promoters, enabling control of strength and timing of

CC heterologous gene expression. The synthetic pox virus promoters that may

CC be used are based on promoters of the vaccinia virus and include early

CC promoter 1 (EPI), late promoter 1 (LPI), EPI and LP2 (AAZ49291-249294,

CC respectively). The recombinant FPV is generated via homologous

CC recombination between FPV DNA and a homology vector containing the

CC foreign DNA flanked by FPV sequences. The recombinant fowlpox viruses of

CC the invention are used as multivalent live vaccines for immunising fowl

CC against Marek's disease virus, NDV, ILTV and/or fowlpox virus. The

CC present sequence represents cDNA encoding NDV haemagglutinin-

CC neuraminidase (HN) and fusion (F) proteins

XX Sequence 4177 BP; 1199 A; 980 C; 910 G; 1088 T; 0 U; 0 Other;

SQ Query Match 51.9%; Score 1741.8; DB 3; Length 4177;

Best Local Similarity 98.8%; Pred. No. 0;

Matches 1755; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 16 TGGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACCTTCTACCAAGAACCC 75

DB 2064 TCGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACCTTCTACCAAGAACCC 2123

QY 76 AGCACCTATGATGCTGACTATCCGGTTCGCTGGCAGTGGTTCATCTGTCCGGCAAA 135

DB 2124 AGACCTATGATGCTGACTATCCGGTTCGCTGGTTCATCTGTCCGGCAAA 2183

QY 136 CTCCATTTGATGGCAGGCTCTTTCGAGCTGCAGGAATTTGGTTTACAGGAGACAAAGCCGT 195

DB 2184 CTCCATTTGATGGCAGGCTCTTTCGAGCTGCAGGAATTTGGTTTACAGGAGACAAAGCAGT 2243

QY 196 CAACATATACCTCATCTCCAGACAGGATCAATATAGTTAAAGTCTCTCCGAATCTGCC 255

DB 2244 CAACATATACCTCATCTCCAGACAGGATCAATATAGTTAAAGTCTCTCCGAATCTGCC 2303

QY 256 CAAGGATAGGAGGATGTGCGAAGCCCTTGGATGATACACAGGACATTTGACAC 315

DB 2304 AAAGGATAAGGAGGATGTGCGAAGCCCTTGGATGATACACAGGACATTTGACAC 2363

QY 316 TTTGTCTCACCCCTTGGTGAATCTATCCGTAGGATCAAGAGTCTGTGACTACATCTGG 375

DB 2364 TTTGTCTCACCCCTTGGTGAATCTATCCGTAGGATCAAGAGTCTGTGACTACATCTGG 2423

QY 376 AGGGGGGAGACAGGGGCGCTTATAGGCGCCATTTATGGCGGTGGTCTTTGGGGTTGC 435

DB 2424 AGGGGGGAGACAGGGGCGCTTATAGGCGCCATTTATGGCGGTGGTCTTTGGGGTTGC 2483

436 AACGCGCACAATAACAGCGCGCGAGCTCTGATACAGCCAAACAAAATGCTGCCAA 495
Dbb
2484 AACGCGCGCACAATAACAGCGCGCGAGCTCTGATACAGCCAAACAAAATGCTGCCAA 2543
Qy CATCTCCGACTTAAAGAGAGCATTGCGCAACCAATGAGGCTGTGATGAGGTCACTGA 555
Dbb
2544 CATCTCCGACTTAAAGAGAGCATTGCGCAACCAATGAGGCTGTGATGAGGTCACTGA 2603
Qy CGGATTATGCAACTAGCAGTGGCAGTTGGGAAGATGACAGCAGTTTGTAAATGACCAATT 615
Dbb
2604 CGGATTATGCAACTAGCAGTGGCAGTTGGGAAGATGACAGCAGTTTGTAAATGACCAATT 2663
Qy TAATAAACAGCTCAGGAATTAGACTGCATCAAAATTTGCACAGCAAGTTGGTGTAGAGCT 675
Dbb
2664 TAATAAACAGCTCAGGAATTAGACTGCATCAAAATTTGCACAGCAAGTTGGTGTAGAGCT 2723
Qy CAACCTGTACCTAACCGAATTGACTACAGTATTCGGACCAACAAATCACTTCACCTGCTTT 735
Dbb
2724 CAACCTGTACCTAACCGAATTGACTACAGTATTCGGACCAACAAATCACTTCACCTGCTTT 2783
Qy 736 AAACAAGCTGACTATTACAGGCACCTTTTAACTCTAGCTGGTGGAAATATGGAATTACTTATT 795
Dbb
2784 AAACAAGCTGACTATTACAGGCACCTTTTAACTCTAGCTGGTGGAAATATGGAATTACTTATT 2843
Qy 796 GACTAAGTTAGGTAGGGAACAATCAACTCAGCTCAATTAATCGGTAGCGCTTTAATCAC 855
Dbb
2844 GACTAAGTTAGGTAGGGAACAATCAACTCAGCTCAATTAATCGGTAGCGCTTTAATCAC 2903
Qy 856 CGGTAAACCTATTCTATACAGCTCACAGACTCAACTCTTGGGTATACAGGTAACTCTACC 915
Dbb
2904 CGGTAAACCTATTCTATACAGCTCACAGACTCAACTCTTGGGTATACAGGTAACTCTACC 2963
Qy 916 TTCAGTCGGGAACCTAAATAATATGCGTGGCCACCTACTTGGAACTTATCGGTAAGCAC 975
Dbb
2964 TTCAGTCGGGAACCTAAATAATATGCGTGGCCACCTACTTGGAACTTATCGGTAAGCAC 3023
Qy 976 AACAGGGGATTGCGTCGGGACCTTGTCCCAAAAGTGGTGACACAGGTGGTTCGTGTAT 1035
Dbb
3024 AACAGGGGATTGCGTCGGGACCTTGTCCCAAAAGTGGTGACACAGGTGGTTCGTGTAT 3083
Qy 1036 AGAAGAACTTGACACCTCATCTATAGAACTGACTAGATTATATGTAACAAGAT 1095
Dbb
3084 AGAAGAACTTGACACCTCATCTATAGAACTGACTAGATTATATGTAACAAGAT 3143
Qy 1096 AGTAAAGTTCCTATGTCCTGCTGATTTATTTCTGCTTGGCGGCAATACGTGGGCTG 1155
Dbb
3144 AGTAAAGTTCCTATGTCCTGCTGATTTATTTACTCTGCTTGGCGGCAATACGTGGGCTG 3203
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Dbb
3204 TATGTACTCAAGACCGAAGGCGCACTTATACACCATATATGACTATCAAAAGGCTCAGT 3263
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Dbb
3264 CATGCCAACTGCAAGATGACAATGTAGATGTAAACCCCGGGGTATCATATCGCA 3323
Qy 1276 AAATATGGAGAAGCGGTGCTCTAAATAGATAAACAATCATGCAATGTTTATCCTTAGG 1335
Dbb
3324 AAATATGGAGAAGCGGTGCTCTAAATAGATAAACAATCATGCAATGTTTATCCTTAGG 3383
Qy 1336 CGGGATAACTTAAAGGCTCAGTGGGGAATTCGATGTAATTCAGAGAATATCTCAAT 1395
Dbb
3384 CGGGATAACTTAAAGGCTCAGTGGGGAATTCGATGTAATTCAGAGAATATCTCAAT 3443
Qy 1396 ACAAGATCTCAAGTAATAATAACAGGCAATCTTGATATCTCACTGAGCTGGGAATGT 1455
Dbb
3444 ACAAGATCTCAAGTAATAATAACAGGCAATCTTGATATCTCACTGAGCTGGGAATGT 3503
Qy 1456 CAACAACCTGATAGTATGCTTTGAATAAGTATAGAGGAAGCAACAGAACTTAGACAA 1515
Dbb
3504 CAACAACCTGATAGTATGCTTTGAATAAGTATAGAGGAAGCAACAGAACTTAGACAA 3563

Qy 1516 AGTCAATGTCAAAGTACTAGCACATCTGCTCTCATTACCTATATCGTTTGTACTATCAT 1575
Dbb
3564 AGTCAATGTCAAAGTACTAGCACATCTGCTCTCATTACCTATATCGTTTGTACTATCAT 3623
Qy 1576 ATCTCTTTGTTTTTGGTATACTTAGCCTGATTTCTAGCATGTCTACCTAATGTACAAGCAAAA 1635
Dbb
3624 ATCTCTTTGTTTTTGGTATACTTAGCCTGATTTCTAGCATGTCTACCTAATGTACAAGCAAAA 3683
Qy 1636 GGCGCAACAAAACCTTTATTTGCTTGGGAATTAATCTTAGATCAGATGAGAGCCAC 1695
Dbb
3684 GGCGCAACAAAACCTTTATTTGCTTGGGAATTAATCTTAGATCAGATGAGAGCCAC 3743
Qy 1696 TACAAAATGTGAACACAGATGAGGAACGAAGGTTTCCCTAAATAGTAATTTGTGTGAAG 1755
Dbb
3744 TACAAAATGTGAACACAGATGAGGAACGAAGGTTTCCCTAAATAGTAATTTGTGTGAAG 3803
Qy 1756 TTCTGGTAGTCTGTCTAGTTCAGAGAGTTAAGAAAAA 1792
Dbb
3804 TTCTGGTAGTCTGTCTAGTTCGGAGAGTTAAGAAAAA 3840

RESULT 13
AAC67862
ID AAC67862 standard; DNA; 4177 BP.
XX AAC67862;
AC AAC67862;
XX
XX 06-AUG-2003 (revised)
DT 02-MAR-2001 (first entry)
XX
XX SfiI fragment comprising NDV HN and F genes.
XX Fowlpox virus; FPV; antiviral; antibacterial; vaccine;
KW Newcastle's disease virus; NDV; Marek's disease;
KW infectious laryngotracheitis; SfiI fragment; HN glycoprotein;
KW F glycoprotein; ds.
XX
XX Newcastle disease virus.
OS
XX
XX US6136318-A.
XX
XX 24-OCT-2000.
PD
XX
XX 07-JUN-1995; 95US-00486414.
PF
XX
XX 26-FEB-1993; 93US-00024156.
PR 28-FEB-1994; 94WO-US002252.
XX
XX (JUNK/) JUNKER D E.
PA (COCH/) COCHRAN M D.
XX
XX Cochran MD, Junker DE;
PI
XX
XX MPI; 2000-686071/67.
DR P-PSDB; AAB36038.
XX
XX New recombinant fowlpox virus useful as vaccines contains foreign DNA
PT inserted into specific non-essential region of the genome.
XX
XX Disclosure; Col 59-68; 56pp; English.
PS
XX
XX The present sequence is provided in a specification relating to a
CC recombinant fowlpox virus (FPV) that comprises a foreign DNA inserted
CC within a 3.5 kb EcoRI fragment of the FPV genomic DNA. The foreign DNA
CC can be expressed in host cells infected with FPV. The recombinant FPV may
CC be used in vaccines to protect animals (especially chickens) against
CC fowlpox and, depending on the source of the foreign DNA, other diseases,
CC particularly Newcastle's disease, Marek's disease or infectious
CC laryngotracheitis. (Updated on 06-AUG-2003 to correct OS field.)
XX
XX Sequence 4177 BP; 1199 A; 980 C; 910 G; 1088 T; 0 U; 0 Other;
SQ

Query Match

51.9%; Score 1741.8; DB 3; Length 4177;

Best Local Similarity 98.8%; Pred. No. 0; Matches 1755; Conservative 0; Mismatches 22; Indels 0; Gaps 0;									
QY	16	TGGATCCCGGTGCGCCCTCCAGGTGCAAGATGGGCTCCAGACCTTCTACCAAGAACCC	75						
Db	2064	TCGATCCCGGTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACCTTCTACCAAGAACCC	2123						
QY	76	AGCACCTATGATGCTGACTATCCGGGTGCGCTGGCACTCAGTTGCATCTGTCCGGCAAA	135						
Db	2124	AGCACCTATGATGCTGACTATCCGGGTGCGCTGGTACTGAGTTGCATCTGTCCGGCAAA	2183						
QY	136	CTCCATTGATGGCAGGCTCTTGAGCTGCAGGAATTGTGGTTACAGGAGACAAAGCCGT	195						
Db	2184	CTCCATTGATGGCAGGCTCTTGAGCTGCAGGAATTGTGGTTACAGGAGACAAAGCAGT	2243						
QY	196	CAACATATACACCTCATCCAGACACGATCAATCATAGTTAAAGCTCTCCGAAATCTGCC	255						
Db	2244	CAACATATACACCTCATCCAGACACGATCAATCATAGTTAAAGCTCTCCGAAATCTGCC	2303						
QY	256	CAAGGATAAGGAGCATGTGCGAAAGCCCTTTGGATGCATACAAACAGGACATTTGACCCAC	315						
Db	2304	AAAGGATAAGGAGCATGTGCGAAAGCCCTTTGGATGCATACAAACAGGACATTTGACCCAC	2363						
QY	316	TTTGCTCACCCCTTTGGTGACTCTATPCGTAGGATACAAAGAGTCTGTGACTACATCTGG	375						
Db	2364	TTTGCTCACCCCTTTGGTGACTCTATPCGTAGGATACAAAGAGTCTGTGACTACATCTGG	2423						
QY	376	AGGGGGAGACAGGGGCGCTTATAGGCGCATATTTGGGGGTGTGGCTCTGGGGTTGC	435						
Db	2424	AGGGGGAGACAGGGGCGCTTATAGGCGCATATTTGGGGGTGTGGCTCTGGGGTTGC	2483						
QY	436	AACTGCGGCACAAATAACAGCGCGCGAGCTCTGTATACAGCCAAACAAAATGCTGCCAA	495						
Db	2484	AACTGCGGCACAAATAACAGCGCGCGAGCTCTGTATACAGCCAAACAAAATGCTGCCAA	2543						
QY	496	CATCCTCCGACTTAAGAGAGCATTTGCCCAACCAATGAGGCTGTGCATGAGGTCACTGA	555						
Db	2544	CATCCTCCGACTTAAGAGAGCATTTGCCCAACCAATGAGGCTGTGCATGAGGTCACTGA	2603						
QY	556	CGGATTTACCAACTAGCAGTGCAGTTGGGAGATGCAGCAGTTTGTAAATGACCAATTT	615						
Db	2604	CGGATTTACCAACTAGCAGTGCAGTTGGGAGATGCAGCAGTTTGTAAATGACCAATTT	2663						
QY	616	TAATAAAACAGCTCAGGAATTAGACTGCATCAAAAATTCACACAAAGTTGGTGTAGAGCT	675						
Db	2664	TAATAAAACAGCTCAGGAATTAGACTGCATCAAAAATTCACACAAAGTTGGTGTAGAGCT	2723						
QY	676	CAACCTGTACCTAACCGAATTGACTACAGTATTCGGACCAACAAATCACTTCACCTGCTTT	735						
Db	2724	CAACCTGTACCTAACCGAATCGACTACAGTATTCGGACCAACAAATCACTTCACCTGCTTT	2783						
QY	736	AAACAAGCTGACTATTTCAGGCACCTTTACAATCTAGCTGGTGGAAATATGGATTACTTATT	795						
Db	2784	AAACAAGCTGACTATTTCAGGCACCTTTACAATCTAGCTGGTGGAAATATGGATTACTTATT	2843						
QY	796	GACTAAGTTAGGTGATGGGAAACAAATCAACTCAGCTCAATTAATCGGTAGCGCTTAATCAC	855						
Db	2844	GACTAAGTTAGGTGATGGGAAACAAATCAACTCAGCTCAATTAATCGGTAGCGCTTAATCAC	2903						
QY	856	CGGTAACCCCTATTCTATACGACTCACAGACTCAACTCTTGGGTATACAGGTAACCTTACC	915						
Db	2904	CGGTAACCCCTATTCTATACGACTCACAGACTCAACTCTTGGGTATACAGGTAACCTTACC	2963						
QY	916	TTCAAGTCGGGAACCTAAATAATATGATGGTGCACCTACTTGGAAACCTTATCCGTAAAGCAC	975						
Db	2964	TTCAAGTCGGGAACCTAAATAATATGATGGTGCACCTACTTGGAAACCTTATCCGTAAAGCAC	3023						
QY	976	AACACAGGGATTTGGCTCGGCACCTTGTCCAAAGTGGTGACACAGGTGGTTCTGTGAT	1035						
Db	3024	AACACAGGGATTTGGCTCGGCACCTTGTCCAAAGTGGTGACACAGGTGGTTCTGTGAT	3083						
QY	1036	AGAAGAACTTGACACCTCTACTGTATAGAAACTGACTTAGATTTATATTGTACAAGAAT	1095						
Db									

3084	AGAAGAACTTGACACCTCTACTGTATAGAAACTGACTTAGATTTATATTGTACAAGAAT	3143
1096	AGTAACGTTCCCTATATCCCTGGTATTTATTCCTCTTGGAGCGCAATACGTCGGCCTG	1155
3144	AGTAACGTTCCCTATATCCCTGGTATTTATTCCTCTTGGAGCGCAATACATCGGCCTG	3203
1156	TATGTACTCAAGACCGAAGCGCACTTACTACACCATATGACTATCAAGGGCTCAGT	1215
3204	TATGTACTCAAGACCGAAGCGCACTTACTACACCATATGACTATCAAGGGCTCAGT	3263
1216	CATCGCAACTGCAAGATGACAACTGTAGATGTGTAAACCCCGGGTATCATATCGCA	1275
3264	CATCGCAACTGCAAGATGACAACTGTAGATGTGTAAACCCCGGGTATCATATCGCA	3323
1276	AAACTATGAGAAGCGCTCTCTAATAGATAAACTCATGCAATGTTATTCCTTAGG	1335
3324	AAACTATGAGAAGCGCTCTCTAATAGATAAACTCATGCAATGTTATTCCTTAGG	3383
1336	CGGGATAACTTTAAGGCTCAGTGGGAATTCGATGTAACTTATCAGAAGAAATATCTCAAT	1395
3384	CGGGATAACTTTAAGGCTCAGTGGGAATTCGATGTAACTTATCAGAAGAAATATCTCAAT	3443
1396	ACAAGATTCCTAAGTAATAATAACAGGCAATCTTGATATCTCACTGAGCTTGGGAATGT	1455
3444	ACAAGATTCCTAAGTAATAATAACAGGCAATCTTGATATCTCACTGAGCTTGGGAATGT	3503
1456	CAACAACTCGATCAAGTAATGCTTGAATAAGTTAGAGGAAGCAACAGAAAACTAGACAA	1515
3504	CAACAACTCGATCAAGTAATGCTTGAATAAGTTAGAGGAAGCAACAGAAAACTAGACAA	3563
1516	AGTCAATGTCAAACTGACTAGCACATCTGCTCTCATTTACCTATATCGTTTGTGACTATCAT	1575
3564	AGTCAATGTCAAACTGACTAGCACATCTGCTCTCATTTACCTATATCGTTTGTGACTATCAT	3623
1576	ATCTCTGTTTGGTATACCTTACCTGATTTAGCATGCTTACCTTAATGTACAGCAAAA	1635
3624	ATCTCTGTTTGGTATACCTTACCTGATTTAGCATGCTTACCTTAATGTACAGCAAAA	3683
1636	GGCGCAACAAAAACCTTATATGCTTGGGAATATATCTAGATCAGATCAGAGCCAC	1695
3684	GGCGCAACAAAAACCTTATATGCTTGGGAATATATCCCTAGATCAGATCAGAGCCAC	3743
1696	TACAAAAATGTGAACAACAGATCAGGAACGAAGGTTTCCCTAATAGTAAATTTGTGTGAAAG	1755
3744	TACAAAAATGTGAACAACAGATCAGGAACGAAGGTTTCCCTAATAGTAAATTTGTGTGAAAG	3803
1756	TTCTGTGATGCTGTCTAGTTTCAGAGAGTTAAGAAAAAA	1792
3804	TTCTGTGATGCTGTCTAGTTTCAGAGAGTTAAGAAAAAA	3840

RESULT 14
ABK90556
ID ABK90556 standard; cDNA; 3570 BP.
XX
AC ABK90556;
XX
DT 15-NOV-2002 (first entry)
XX
DE Newcastle disease virus (NDV) fusion gene.
XX
KW Newcastle disease virus; gene; ss; novel recombinant avian herpesvirus;
KW NAHV, herpes virus of turkeys; HVT; Marek's disease; Newcastle disease;
KW infectious laryngotracheitis; virucide; immunostimulant; vaccine; NDV.
XX
OS Newcastle disease virus.
XX
FH Key Location/Qualifiers
FT CDS 1194..2888
FT /tag= a
FT /product= "Newcastle disease virus protein"
FT /transl_except= (pos:1353..1355, aa:Xaa)
FT /note= "Xaa= unknown"

XX PN US2002081316-A1.
XX PD 27-JUN-2002.
XX PP 14-JUN-2001; 2001US-00881457.
XX PR 12-JUN-1992; 92US-00898087.
XX PR 26-FEB-1993; 93US-00023610.
XX PR 14-JUN-1993; 93WO-US005681.
XX PR 09-AUG-1994; 94US-00288065.
XX PR 09-AUG-1995; 95WO-US010245.
XX PR 13-JUN-1996; 96US-00663566.
XX PR 21-FEB-1997; 97US-00804372.
XX PR 25-OCT-1999; 99US-00426352.
XX (COCH/) COCHRAN M D.
XX PA (COOK/) COOK S M.
XX PA (WILD/) WILD M A.
XX PI Cochran MD, Cook SM, Wild MA;
XX DR WPI; 2002-635456/68.
XX DR P-PSDB; ABG31709.
XX XX Novel recombinant avian herpesvirus comprising unique long and repeat
PT viral genome regions of herpes virus of turkeys, unique short viral
PT genome region of Marek's disease virus, and optional foreign DNA
PT sequence.
XX XX Disclosure; Page 12-14; 26pp; English.
XX CC The invention relates to a novel recombinant avian herpesvirus (NAHV)
CC comprising a herpes virus of turkeys (HVT) unique long (UL) and repeat
CC viral genome region and a Marek's disease virus unique short (US) viral
CC genome region where at least one foreign DNA sequence is inserted within
CC a US2 gene of the US region of the NAHV, and is capable of being
CC expressed in a host cell. NAHV is useful for producing vaccines used for
CC immunising an avian species against Newcastle disease, infectious
CC laryngotracheitis and Marek's disease. This sequence represents a
CC Newcastle disease virus (NDV) fusion gene
XX SQ Sequence 3570 BP; 982 A; 857 C; 845 G; 885 T; 0 U; 1 Other;
Query Match 50.7%; Score 1701.6; DB 6; Length 3570;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 1749; Conservative 0; Mismatches 25; Indels 3; Gaps 3;
QY 16 TGGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACCTTCTACCAAGAACCC 75
DB 1199 TCGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACCTTCTACCAAGAACCC 1258
QY 76 AGCACTATGATGCTGACTATCCGGGTTGGCTGGCACTGAGTTGCATCTGTCCGGCAAA 135
DB 1259 AGCACTATGATGCTGACTATCCGGGTTGGCTGGCACTGAGTTGCATCTGTCCGGCAAA 1318
QY 136 CTCATTGATGGCAGGCTCTTGCACTGCAAGGAATTTGGTTACAGGACCAAGCCGT 195
DB 1319 CTCATTGATGGCAGGCTCTTGCACTGCAAGG-ACTNTGTTACAGGACCAAGCAAT 1377
QY 196 CAACATATACCTTCATCCAGACAGGATCAATCATAGTTAAGTCTCTCCGATCTGCC 255
DB 1378 CAACATATACCTTCATCCAGACAGG-TCAATCATAT-TTAAGTCTCTCCGATCTGCC 1435
QY 256 CAAGGATAAGGAGCATGTGCAAGCCCTTGGATGCATACAAAGGACATTGACCA 315
DB 1436 AAGGATTAAGGAGCATGTGCAAGCCCTTGGATGCATACAAAGGACATTGACCA 1495
QY 316 TTTGCTCACCCCTTGGTGAATCTATCCGTAGGATACAAAGAGTCTGTGACTACATCTGG 375
DB 1496 TTTGCTCACCCCTTGGTGAATCTATCCGTAGGATACAAAGAGTCTGTGACTACATCTGG 1555
QY 376 AGGGGGAGACAGGGGGCCCTTATAGGGCCCATTAATTTGGCGGTGTGGCTCTTGGGGTTGC 435

DB 1556 AGGGGGAGACAGGGGGCCCTTATAGGGCCATTAATTTGGCGGTGTGGCTCTTGGGGTTGC 1615
QY 436 AACTGCCGCAAAATAACAGCGCCGAGCTCTGTATACAAAGCCAAAATAAATGTGCAAA 495
DB 1616 AACTGCCGCAAAATAACAGCGCCGAGCTCTGTATACAAAGCCAAAATAAATGTGCAAA 1675
QY 496 CATCTCCGACTTAAAGAGAGCATTGGCGCAACCAATGAGGCTGTGATGAGGTCACTGA 555
DB 1676 CATCTCCGACTTAAAGAGAGCATTGGCGCAACCAATGAGGCTGTGATGAGGTCACTGA 1735
QY 556 CGGATTATCGCACTAGCAGTGGCAGTTGGGAAGATGACAGCAGTTGTTAATGACCAATT 615
DB 1736 CGGATTATCGCACTAGCAGTGGCAGTTGGGAAGATGACAGCAGTTGTTAATGACCAATT 1795
QY 616 TAATAAAACAGCTCAGGAATTAGATCGCATCAAAATTTGCAAGAGTTGGTGTAGAGCT 675
DB 1796 TAATAAAACAGCTCAGGAATTAGATCGCATCAAAATTTGCAAGAGTTGGTGTAGAGCT 1855
QY 676 CAACCTGTACTTAACCGAATTGACTACAGTATTCGGACCAAAATCACTTCACTGCTTT 735
DB 1856 CAACCTGTACTTAACCGAATTGACTACAGTATTCGGACCAAAATCACTTCACTGCTTT 1915
QY 736 AAACAAGCTGACTTATTCAGGCACCTTTACAATCTAGCTGGTGGAAATATGGAATTAATT 795
DB 1916 AAACAAGCTGACTTATTCAGGCACCTTTACAATCTAGCTGGTGGAAATATGGAATTAATT 1975
QY 796 GACTAAGTTAGTTAGTGGGAACCAATCAACTCAGCTCAATTAATCGGTAGCGGCTTAATCAC 855
DB 1976 GACTAAGTTAGTTAGTGGGAACCAATCAACTCAGCTCAATTAATCGGTAGCGGCTTAATCAC 2035
QY 856 CGGTAAACCTTATCTATACGACTCAGACACTCAACTCTTGGGTATACAGTAACTCTACC 915
DB 2036 CGGTAAACCTTATCTATACGACTCAGACACTCAACTCTTGGGTATACAGTAACTCTACC 2095
QY 916 TTCACTCGGGAACCTTAATAATATGCTGCGCACCTACTTGGAAACCTTATCCGTAAGCAC 975
DB 2096 TTCACTCGGGAACCTTAATAATATGCTGCGCACCTACTTGGAAACCTTATCCGTAAGCAC 2155
QY 976 AACCAGGGGATTTGCTTCGGCCTTGTCCCAAAAGTGGTGACACAGTCGGTCTGTGAT 1035
DB 2156 AACCAGGGGATTTGCTTCGGCCTTGTCCCAAAAGTGGTGACACAGTCGGTCTGTGAT 2215
QY 1036 AGAAGAACTTGACACCTCATCTGTATAGAACTGACTTGAATTTATTTGTACAAAGAT 1095
DB 2216 AGAAGAACTTGACACCTCATCTGTATAGAACTGACTTGAATTTATTTGTACAAAGAT 2275
QY 1096 AGTAACGTTCCCTATGTCCCTGTTATTTATTTCTGCTTCAGGGGCAATAGCTGGGCTG 1155
DB 2276 AGTAACGTTCCCTATGTCCCTGTTATTTATTTCTGCTTCAGGGGCAATAGCTGGGCTG 2335
QY 1156 TATGTACTCAAAGACCGAAGCGCCTTACTACACCATACATGACTATCAAAGGTTTCACT 1215
DB 2336 TATGTACTCAAAGACCGAAGCGCCTTACTACACCATATATGACTATCAAAGGCTCAGT 2395
QY 1216 CATCGCCAACTGCAAGATGACAACTGATGTGTAAACCCCGGGGTATCATATCGCA 1275
DB 2396 CATCGCTAACTGCAAGATGACAACTGATGTGTAAACCCCGGGGTATCATATCGCA 2455
QY 1276 AACTATGGAGAGCGGCTGCTCTTAATAGATAAACCAATCATGCAATGTTTATCTCTTAGG 1335
DB 2456 AACTATGGAGAGCGGCTGCTCTTAATAGATAAACCAATCATGCAATGTTTATCTCTTAGG 2515
QY 1336 CGGGATAAATTTTAAGGCTCAGTGGGAATTCGATGTAACTTATCAGAGAATATCTCAAT 1395
DB 2516 CGGGATAAATTTTAAGGCTCAGTGGGAATTCGATGTAACTTATCAGAGAATATCTCAAT 2575
QY 1396 ACAAGATTCTCAAGTAATAATAACAGCAATCTTTGATATCTCACTGAGCTTGGGAATGT 1455
DB 2576 ACAAGATTCTCAAGTAATAATAACAGCAATCTTTGATATCTCACTGAGCTTGGGAATGT 2635
QY 1456 CAACAATCGATCAGTAATGCTTTGATAGATTAGGGAAGCAACAGAAATCTAGACAA 1515

Db 2636 CAACTCGATCAGTAATGCTTGAATAGTTAGAGAAAGCAACAGAAAACTAGACAA 2695
QY 1516 AGTCAATGTCACACTGACATGACATCTGCTCATTTACTATATGCTTTTGACTATCAT 1575
Db 2696 AGTCAATGTCACACTGACATGACATCTGCTCATTTACTATATGCTTTTGACTATCAT 2755
QY 1576 ATCTCTGTTTGGTATACCTTAGCCCTGATTTCTAGCATGCTACTTAATGTACAAGCAAAA 1635
Db 2756 ATCTCTGTTTGGTATACCTTAGCCCTGATTTCTAGCATGCTACTTAATGTACAAGCAAAA 2815
QY 1636 GGGCAACAAAAACCTTATATGCTTGGGAATAATATCTTAGATCAGATGAGAGCCAC 1695
Db 2816 GGGCAACAAAAAGACCTTATATGCTTGGGAATAATATCTTAGATCAGATGAGAGCCAC 2875
QY 1696 TACAAAAATCTGAACACAGATGAGGACGAAGGTTTCCCTAATAGTAATTTGTGTGAAG 1755
Db 2876 TACAAAAATGTGAACACAGATGAGGACGAAGGTTTCCCTAATAGTAATTTGTGTGAAG 2935
QY 1756 TTCTGCTAGTCTGCTAGTTTCAGATTCAGAGAGTTAAGAAAAAA 1792
Db 2936 TTCTGCTAGTCTGCTAGTTTCAGATTCAGAGAGTTAAGAAAAAA 2972

RESULT 15
AAT18203
ID AAT18203 standard; DNA; 1662 BP.
AC AAT18203;
XX
DT 04-MAR-1997 (first entry)
XX
DE Newcastle disease virus F gene.
XX
KW Turkey herpes virus; recombinant virus; vaccine; prophylaxis;
KW immunisation; avian virus; infectious bronchitis virus;
KW infectious bursal disease virus; Newcastle disease virus;
KW Marek's disease virus; infectious laryngotracheitis virus; IBV; IBDV;
KW NDV; MDV; ILV; ds.
XX
OS Newcastle disease virus.
XX
FH Key Location/Qualifiers
FT 1. 1662
FT CDS /tag= a
FT /product= "NDV F gene product"
XX
PN W09605291-A1.
XX
XP 22-FEB-1996.
XX
XP 09-AUG-1995; 95WO-US010245.
XX
XP 09-AUG-1994; 94US-00288065.
PR 22-DEC-1994; 94US-00362240.
XX
XX (SYTR) SYNTRO CORP.
XX
PI Cochran MD, Junker DE, Wild MA, Singer PA;
XX
DR WPI; 1996-139689/14.
DR P-PSDB; AAW06828.
XX
XX Recombinant turkey herpes viruses contg. foreign DNA encoding a cytokine
PT - useful in vaccines to protect against Marek's disease virus and other
PT avian viruses.
XX
PS Disclosure; Page 177-179; 249pp; English.
XX
CC Recombinant turkey herpes virus (rTH) which comprise a foreign DNA
CC sequence encoding a cytokine inserted into a XhoI site within an EcoRI #9
CC genomic fragment, where the cytokine can be expressed in host cells
CC infected with the virus can be used in vaccines to protect turkeys
CC against avian viruses. The recombinant viruses can be used for immunising

CC birds against infectious bronchitis virus (IBV), infectious bursal
CC disease virus (IBDV), Marek's disease virus (MDV) infectious
CC laryngotracheitis virus (ILV) and Newcastle disease virus (NDV). They may
CC also be used in multivalent vaccines to protect against two or more of
CC these avian viruses. This sequence is the F gene of the Newcastle disease
CC virus and encodes an antigen which can be used in the recombinant
CC vaccines
XX
SQ Sequence 1662 BP; 507 A; 390 C; 353 G; 412 T; 0 U; 0 Other;
Query Match 48.6%; Score 1631.6; DB 2; Length 1662;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 1643; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 47 ATGGGCTCCAGACCTTTACCAAGAACCCAGACACCTATGATGCTGACTATCCGGGTTCGG 106
Db 1 ATGGGCTCCAGACCTTTACCAAGAACCCAGACACCTATGATGCTGACTATCCGGGTTCGG 60
QY 107 CTGGCACTGAGTTGCATCTGTCCGGCAAACTCCATTTGATGGCAGGCTCTTGCACTGCA 166
Db 61 CTGGTACTGAGTTGCATCTGTCCGGCAAACTCCATTTGATGGCAGGCTCTTGCACTGCA 120
QY 167 GGAATTTGGTTACAGGAGACAAGCCGTCAACATATACACCTCATCCAGACAGATCA 226
Db 121 GGAATTTGGTTACAGGAGACAAGCCGTCAACATATACACCTCATCCAGACAGATCA 180
QY 227 ATCATAGTTAAGCTCTCCCGAATCTGCCAAGGATAAGGAGGCATGTGCGAAAGCCCC 286
Db 181 ATCATAGTTAAGCTCTCCCGAATCTGCCAAGGATAAGGAGGCATGTGCGAAAGCCCC 240
QY 287 TTGGATGCATACAACAGGACATTTGACCACTTTTGCTCACCCCCCTTGGTGACTCTATCCGT 346
Db 241 TTGGATGCATACAACAGGACATTTGACCACTTTTGCTCACCCCCCTTGGTGACTCTATCCGT 300
QY 347 AGATAACAAGAGTCTGTGACTACATCTGGAGGGGAGACAGGGGGCCTTATAGCGGCC 406
Db 301 AGGATAACAAGAGTCTGTGACTACATCTGGAGGGGAGACAGGGGGCCTTATAGCGGCC 360
QY 407 ATTATTTGGGGTGTGGCTCTTGGGGTTGCAACTGCGGCACAAATAACAGCGGCGCAGCT 466
Db 361 ATTATTTGGGGTGTGGCTCTTGGGGTTGCAACTGCGGCACAAATAACAGCGGCGCAGCT 420
QY 467 CTGATAACAAGCCAAACAAAATGCTGCCAACATCTCTCCGACTTAAAGAGAGCATTTGCCGA 526
Db 421 CTGATAACAAGCCAAACAAAATGCTGCCAACATCTCTCCGACTTAAAGAGAGCATTTGCCGA 480
QY 527 ACCAATGAGGCTGTGCATGAGGTCACTGACGAGTTATCCGAACCTAGCAGTGGCAGTTGG 586
Db 481 ACCAATGAGGCTGTGCATGAGGTCACTGACGGATTATCGCAACTAGCAGTGGCAGTTGG 540
QY 587 AAGATGCAGCAGTTTGTTAATGACCAATTTAATAAAACAGCTCAGGAATTAGACTGCATC 646
Db 541 AAGATGCAGCAGTTTGTTAATGACCAATTTAATAAAACAGCTCAGGAATTAGACTGCATC 600
QY 647 AAAAATGCACAGCAAGTTGGTGTAGAGCTCAACCTGTACTTAACCGAATTTGACTACAGTA 706
Db 601 AAAAATGCACAGCAAGTTGGTGTAGAGCTCAACCTGTACTTAACCGAATTTGACTACAGTA 660
QY 707 TTCGGACCAAAAATCACTTCACCTGTTTAAACAAGCTGACTATTTCAGGCACTTTTCAAT 766
Db 661 TTCGGACCAAAAATCACTTCACCTGTTTAAACAAGCTGACTATTTCAGGCACTTTTCAAT 720
QY 767 CTAGCTGGTGGAAATATGATTACTTATTGACTTAAGTTAGGTGATGGGAACCAATCAACTC 826
Db 721 CTAGCTGGTGGAAATATGATTACTTATTGACTTAAGTTAGGTGATGGGAACCAATCAACTC 780
QY 827 AGCTCAATTAATCGGTAGCGGCTTAATCAGCGGTAAACCTTATTCATACGACTCACAGACT 886
Db 781 AGCTCAATTAATCGGTAGCGGCTTAATCAGCGGTAAACCTTATTCATACGACTCACAGACT 840
QY 887 CAACTCTTGGGTATACAGGTAACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTAC 946
Db 841 CAACTCTTGGGTATACAGGTAACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTAC 900

Qy	947	ACCTACTTGGAAACCTTATCCGTAAGCAAAACAGGGGATTTGCTCGGCACTTGTGCCA	1006
Db	901	ACCTACTTGGAAACCTTATCCGTAAGCAAAACAGGGGATTTGCTCGGCACTTGTGCCA	960
Qy	1007	AAAGTGGTGACACAGGTGGTTCTGTATAGAACTTGACACCTCATCTGTATAGAA	1066
Db	961	AAAGTGGTGACACAGGTGGTTCTGTATAGAACTTGACACCTCATCTGTATAGAA	1020
Qy	1067	ACTGACTTAGATTATATTTGTAAGAATAGTAAGTTCCCTATGTCCCTGGTATTAT	1126
Db	1021	ACTGACTTAGATTATATTTGTAAGAATAGTAAGTTCCCTATGTCCCTGGTATTAT	1080
Qy	1127	TCCTGCTTGGCGGCAATACGTGGGCTGTATGTACTCAAGACCGAAGGCGCACTTACT	1186
Db	1081	TCCTGCTTGGCGGCAATACGTGGGCTGTATGTACTCAAGACCGAAGGCGCACTTACT	1140
Qy	1187	ACACCATACATGACTATCAAGGTTTCAGTCAATCGCAACTGCAAGATGCAACAATGTAGA	1246
Db	1141	ACACCATACATGACTATCAAGGTTTCAGTCAATCGCAACTGCAAGATGCAACAATGTAGA	1200
Qy	1247	TGTGTAAACCCCGGGTATCATATCGCAAACTATGGAGAGCGGTCTCTTAATAGAT	1306
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Db	1321	GATGTAACCTATCAGAGAATATCTCAATACAAGATTTCAAGTAATAATAACAGGCAAT	1380
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Db	1561	CTAGCATGCTACCTAAATGTAAGCAAGGCGCAACAAAGACCTTATTATGCTTGGG	1620
Qy	1667	AATAATCTCTAGATCAGATGAGGCCACTACAAAAATGTGA	1708
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Job time : 1709 secs

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OM nucleic - nucleic search, using sw model

Run on: October 1, 2005, 11:20:23 ; Search time 535 Seconds
(without alignments)
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Title: US-10-800-256-1

Perfect score: 3358

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3353.2	99.9	15186	4 US-09-741-744A-134	Sequence 134, Appl
2	3196.4	95.2	3825	6 5310678-2	Patent No. 5310678
3	3196.4	95.2	3825	6 5310678-2	Patent No. 5310678
4	1741.8	51.9	4177	2 US-08-484-575A-12	Sequence 12, Appl
5	1741.8	51.9	4177	3 US-08-477-459-12	Sequence 12, Appl
6	1741.8	51.9	4177	3 US-08-479-869-12	Sequence 12, Appl
7	1741.8	51.9	4177	3 US-08-486-414-12	Sequence 12, Appl
8	1741.8	51.9	4177	5 PCT-US94-01826A-12	Sequence 12, Appl
9	1741.8	51.9	4177	5 PCT-US94-02252A-12	Sequence 12, Appl
10	1631.6	48.6	1662	2 US-08-663-566A-12	Sequence 12, Appl
11	1631.6	48.6	1662	2 US-08-023-610-12	Sequence 12, Appl
12	1631.6	48.6	1662	2 US-08-288-065A-12	Sequence 12, Appl
13	1631.6	48.6	1662	2 US-08-362-240A-12	Sequence 12, Appl
14	1631.6	48.6	1662	3 US-08-804-372A-10	Sequence 10, Appl
15	1631.6	48.6	1662	5 PCT-US95-10245-12	Sequence 12, Appl
16	1511	45.0	1907	1 US-07-820-154A-29	Sequence 29, Appl
17	1511	45.0	1907	2 US-08-097-554A-29	Sequence 29, Appl
18	1511	45.0	1907	3 US-08-480-640A-29	Sequence 29, Appl
19	1511	45.0	1907	3 US-08-295-802-29	Sequence 29, Appl
20	1511	45.0	1907	3 US-08-488-237A-29	Sequence 29, Appl
21	1511	45.0	1907	3 US-08-375-992A-29	Sequence 29, Appl
22	1511	45.0	1907	4 US-08-472-679H-29	Sequence 29, Appl
23	1511	45.0	1907	5 PCT-US93-00324-29	Sequence 29, Appl
24	1448	43.1	2176	1 US-07-778-890A-2	Sequence 2, Appl
25	1421.6	42.3	1734	2 US-08-663-566A-10	Sequence 10, Appl
26	1421.6	42.3	1734	2 US-08-023-610-10	Sequence 10, Appl
27	1421.6	42.3	1734	2 US-08-288-065A-10	Sequence 10, Appl

28	1421.6	42.3	1734	2	US-08-362-240A-10	Sequence 10, Appl
29	1421.6	42.3	1734	3	US-08-804-372A-8	Sequence 8, Appl
30	1421.6	42.3	1734	5	PCT-US95-10245-10	Sequence 10, Appl
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33	1368.4	40.8	2521	2	US-08-578-096A-18	Sequence 18, Appl
34	1368.4	40.8	2521	3	US-08-790-517-8	Sequence 8, Appl
35	1368.4	40.8	2521	3	US-09-240-426-18	Sequence 18, Appl
36	1368.4	40.8	2521	3	US-09-219-932-14	Sequence 14, Appl
37	1368.4	40.8	2521	3	US-09-362-831-8	Sequence 8, Appl
38	1362.8	40.6	1662	3	US-09-232-479-10	Sequence 10, Appl
39	1362.8	40.6	1662	3	US-09-784-990-10	Sequence 10, Appl
40	1160.8	34.6	1716	3	US-09-232-479-7	Sequence 7, Appl
41	1160.8	34.6	1716	3	US-09-784-990-7	Sequence 7, Appl
42	127.2	3.8	1685	1	US-08-105-483-370	Sequence 370, App
43	127.2	3.8	1685	1	US-08-709-209-370	Sequence 370, App
44	127.2	3.8	1685	1	US-08-458-101-370	Sequence 370, App
45	120.2	3.6	1656	2	US-08-700-548-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-09-741-744A-134
; Sequence 134, Application US/09741744A
; Patent No. 6719979
; GENERAL INFORMATION:
; APPLICANT: Peeters, Bernadus
; APPLICANT: de Leeuw, Olav
; APPLICANT: Klaus, Gius
; APPLICANT: Arnoud, Gielkens
; TITLE OF INVENTION: Newcastle Disease Virus Infectious Clones, Vaccines and Diagnosti
; FILE REFERENCES: 2183-4646US
; CURRENT APPLICATION NUMBER: US/09/741,744A
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: PCT/NL99/00377
; PRIOR FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 134
; LENGTH: 15186
; TYPE: DNA
; ORGANISM: Newcastle disease virus LaSota
US-09-741-744A-134

Query Match	99.9%	Score 3353.2;	DB 4;	Length 15186;
Best Local Similarity	99.9%	Pred. No. 0;		
Matches 3353;	Conservative	0;	Mismatches 3;	Indels 0;
Gaps 0;				
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Qy	61	TTCTACCAAGAACCCAGCAGCCTATGATGCTGATATCCGGTTGCGGTGCGCTGACGTAGTTG	120	
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Qy	301	CAGGACATTCACCACTTTGCTACCCCTTGGTACTCTATCCGTAGGATACAAGATC	360	
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QY	541	GCATGAGGTCACTGACGGATTAATCGCAATAGCAGTGGCAGTTGGGAAGATGACGAGTT	600
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Db	5998	CAGAAACTAGACAAAGTCAATGTCTAAACCTGACTAGCACATCTGCTCTCATTTACCTATAT	6057
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Db	6178	TCAGATGAGAGCCACTACAAAAATGTGAACACAGATGAGGAACGAAGTTTCCCTAATAG	6237
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Qy 2761 GAAAGGACCTAGATGTACAACTATTCGGGAGTGGTGGCCAACTACCCAGGAGTA 2820
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Db 7798 AACTCGTGTGTTACTGGAGTCTATACAGATCCATCCCTTAATCTTCTATAGAAACC 7855
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RESULT 2

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5310678-2
; Patent No. 5310678
; APPLICANT: Bingham, Richard W.; Chambers, Phillip; Emmerson, Peter
; T.; Millar, Neil S.
; TITLE OF INVENTION: NEWCASTLE DISEASE VIRUS GENE CLONES
; NUMBER OF SEQUENCES: 3
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/438,945
; FILING DATE: 17-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 885,765
; FILING DATE: 15-JUL-1986
; SEQ ID NO: 2
; LENGTH: 3825
5310678-2
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Query Match 95.2%; Score 3196.4; DB 6; Length 3825;
Best Local Similarity 97.0%; Pred. No. 0;
Matches 3257; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

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Db 841 TAGCGGCTTAATCAACCGGTAAACCTATTCATACGACTCAGACTCAACTCTTTGGGTAT 900
Qy 901 ACAGGTAACTCTACCTTCAGTCCGGAACCTAAATATATGCGTCCACCTACTCTTGGAAAC 960
Db 901 ACAGGTAACTCTACCTTCAGTCCGGAACCTAAATATATGCGTCCACCTACTCTTGGAAAC 960
Qy 961 CTTATCCGTAAAGCAACACAGGGGATTTGGCTCGGCACTTTGTCCCAAAAGTGGTGACACA 1020
Db 961 CTTATCTGTAAAGCAACACAGGGGATTTGGCTCGGCACTTTGTCCCAAAAGTGGTGACACA 1020
Qy 1021 GGTGGGTTCTGTGATAGAGAACTTGACA CTTCTATCTGTATAGAAACTGACTTAGATTTT 1080
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Db	1021	GGTCGGTCTGTGATAGAGAACTTGACCTCATATTGTATAGAAACCGACTTGAATTT	1080
Qy	1081	ATATTGTACAAGATAGTAAGCTTCCCTATGTCCCTCGTATTTATTCCTGCTTGAGCGG	1140
Db	1081	ATATTGTACAAGATAGTAAGCTTCCCTATGTCCCTCGTATTTATTCCTGCTTGAGCGG	1140
Qy	1141	CAATACGTCGGCTGTATGTACTCAAAAGACGGAAGGCGCACTTACTACACATACATGAC	1200
Db	1141	CAATACATCGGCTGTATGTACTCAAAAGACGGAAGGCGCACTACTACGCCATACATGAC	1200
Qy	1201	TATCAAGGTTCACTATCGCCCACTGCAAGATGACAAAGTGTAGATGTGTAAACCCCC	1260
Db	1201	TATCAAGGTTCACTATCGCCCACTGCAAGATGACAAAGTGTAGATGTGTAAACCCCC	1260
Qy	1261	GGGTATCATATCGCAAACTATGAGAAAGCGGTGCTCTTAATAGATAAAACAATCATGCAA	1320
Db	1261	GGGTATCATATCGCAAACTATGAGAAAGCGGTGCTCTTAATAGATAAGCAATCATGCAA	1320
Qy	1321	TGTTTTATCCTTAGCGGGGATAAATTTAAGGCTCAGTGGGGAATTCGATGAACCTTATCA	1380
Db	1321	TGTTTTATCCTTAGCGGGGATAAATTTAAGGCTCAGTGGGGAATTCGATGAACCTTATCA	1380
Qy	1381	GAAGAATATCTCAATACAGATCTCAAGTAATAAATCAAGGCAATCTTGATATCTCAAC	1440
Db	1381	GAAGAATATCTCAATACAGATCTCAAGTAATAAATCAAGGCAATCTTGATATCTCAAC	1440
Qy	1441	TGAGCTTGGGAATGTCAAACTCGATCAGTAATGCTTTCGAATAAGTTAGAGGAAGCAA	1500
Db	1441	TGAGCTTGGGAATGTCAAACTCGATCAGTAATGCTTTCGAATAAGTTAGAGGAAGCAA	1500
Qy	1501	CAGAAAACCTAGACAAAGTCAATGTCAAACTGACTAGCACATCTGCTCTCAATTACCTATAT	1560
Db	1501	CAGAAAACCTAGACAAAGTCAATGTCAAACTGACCCAGCACATCTGCTCTCAATTACCTATAT	1560
Qy	1561	CGTTTGAACATCATATCTCTGTTTGGTATATCTTAGCTGATTTAGCATGTCTACCT	1620
Db	1561	CGTTTGAACATCATATCTCTGTTTGGTATATCTTAGCTGATTTAGCATGTCTACCT	1620
Qy	1621	AATGTACAAGCAAAAGCGCAACAAAAACCTTATTATGCTTGGGAATAATACTCTAGA	1680
Db	1621	AATGTACAAGCAAAAGCGCAACAAAAACCTTATTATGCTTGGGAATAATACTCTAGA	1680
Qy	1681	TCAGATGAGAGCCACTACAAAAATGTGAACACAGATGAGGAACGAAGTTTCCCTAATAG	1740
Db	1681	TCAGATGAGAGCCACTACAAAAATGTGAACACAGATGAGGAACGAAGTTTCCCTAATAG	1740
Qy	1741	TAATTTGTGTGAAGTTCTGGTAGTCTGTCAAGTTCAAGATTTAAGAAAAAATACCGGT	1800
Db	1741	TAATTTGTGTGAAGTTCTGGTAGTCTGTCAATTTCCGAGAGTTTGAAAAAAATACCGGT	1800
Qy	1801	TGTAGATGACCAAGGACGATATACGGGTAGAACGGTAAAGAGGCGCCCTCAATTGC	1860
Db	1801	TGTAGATGACCAAGGACGATATACGGGTAGAACGGTAAAGAGGCGCCCTCAATTGC	1860
Qy	1861	GAGCAGGCTTCAAACTCCGTTCTACCGGTTCAACGCAACAGTCCCTCAATCATGGAC	1920
Db	1861	GAGCAGGCTTCAAACTCCGTTCTACCGTTCAACGCAACAGTCCCTCAGTCATGGAC	1920
Qy	1921	CGGCGGTTAGCCAAAGTTGGTTAGAGAAATGATGAAGAGGCAAAAAATACATGGCGC	1980
Db	1921	CGGCGGTTAGCCAAAGTTGGTTAGAGAAATGATGAAGAGGCAAAAAATACATGGCGC	1980
Qy	1981	TTGATATTCGGATTGCAATCTTATCTTAACAGTAGTACCTTGGCTATATCTGTAGCC	2040
Db	1981	TTGATATTCGGATTGCAATCTTACTCTTAACAGTAGTACCTTGGCTATATCTGTAGCC	2040
Qy	2041	TCCCTTTATATAGCATGGGGCTAGCACACCTAGCGATCTTGTAGGCATACCGACTAGG	2100
Db	2041	TCCCTTTGTAATAGCATGGGGCTAGCACACCTAGCGACCTTGTAGGCATACCGACGAGG	2100
Qy	2101	ATTTCCAGGCGAGNAGAAAGATTACATCTACACTTGGTTCCAAATCAAGATGTAGTAGAT	2160

Db	2101	ATTTCTAGGGCAGAGAAAAGATTACATCTGCACCTTGGTTCCAAATCAAGATGTAGTAGAT	2160
Qy	2161	AGGATATATAAGCAAGTGGCCCTTGAGTCTCCGTTGGCATTTGTTAAATACTAGACACACA	2220
Db	2161	AGGATATATAAGCAAGTGGCCCTTGAGTCTCCGTTGGCATTTGTTAAATACTAGACACACA	2220
Qy	2221	ATTATGAACGCAATAACATCTCTCTTATCAGATTAATTTGGAGCTGCAACACAGTGGG	2280
Db	2221	ATTATGAACGCAATAACATCTCTCTTATCAGATTAATTTGGAGCTGCAACACAGCGGG	2280
Qy	2281	TGGGGGSCACCTTATCCATGACCCAGATTATATAGGGGGGATAGGCAAAAGAACTCATTTGA	2340
Db	2281	TGGGGGSCACCTTATCCATGACCCAGATTATATCGGGGGGATAGGCAAAAGAACTCATTTGA	2340
Qy	2341	GATGATGCTAGTGAATGTCATCATCTATCCCTCTGCAATTTCAAGAAACATCTGAATTTT	2400
Db	2341	GATGATGCTAGTGAATGTCATCATCTATCCCTCTGCAATTTCAAGAAACATCTGAATTTT	2400
Qy	2401	ATCCCGGCGCTACTACAGGATCAGGTTGGACATCTCGAATACCCCTCATTTGACATGAGTGT	2460
Db	2401	ATCCCGGCGCTACTACAGGATCAGGTTGGACATCTCGAATACCCCTCATTTGACATGAGTGT	2460
Qy	2461	ACCCATTTACTGTACACCCCATTAATGTAATATTGTTGTTGATGAGAGATCACTCACATTC	2520
Db	2461	ACCCATTTACTGTACACTCATTAATGTAATATTGTTGTTGATGAGAGATCACTCACATTC	2520
Qy	2521	TATCAGTATTTAGCACTTGGTGTCTCCGGAACATCTGCAACAGGGAGGGTATTTCTTTTCT	2580
Db	2521	CATCAGTATTTAGCACTTGGTGTCTCCGGAACATCTGCAACAGGGAGGGTATTTCTTTTCT	2580
Qy	2581	ACTCTCGGTTCCATCAACCTGGACGACACCCAAAATCGGAAATCTTTCAGTGTGAGTGA	2640
Db	2581	ACTCTCGGTTCCATCAGTCTGGATGACAGCCAAAATCGGAAATCTTTCAGTGTGAGTGA	2640
Qy	2641	ACTCCCTCGGTTGATATGCTGCTCGAAGTCAACGAGACACAGGAAGAAAGATTAT	2700
Db	2641	ACTCCCTTAGGTTGATATGCTGCTCGAAGTCAACGAGACACAGGAAGAAAGATTAT	2700
Qy	2701	AACTCAGCTGTCCCTACGGGATGTTACATGGAGGTTAGGGTTCCAGCGGCCAGTACCAC	2760
Db	2701	AACTCAGCTGTCCCTACGGTATGGACATGGAGGTTAGGGTTCCAGCGGCCAATACCAC	2760
Qy	2761	GAAAAGGACTAGATGTCTCAACATTTTCGGGACTGGGTGGCCAACTACCCAGAGTA	2820
Db	2761	GAAAAGGACTAGACGTCTCAACATTTTTAGGACTGGGTGGCCAACTACCCAGAGTA	2820
Qy	2821	GGGGTGGATCTTTTATTCACAGCGGTATGTTCTCAGTCTACGAGGTTTAAACCC	2880
Db	2821	GGGGTGGATCTTTTATTCACGCGCGGTATGTTCTCAGTCTACGAGGCTGAAACCC	2880
Qy	2881	AAATTCACCCAGTGACACTGTACAGGAAGGAAATATGTGATATACAAAGCGATACAAATGAC	2940
Db	2881	AAATTCACCCAGTGACACTGTACAGGAAGGAAATATGTAAATATACAAAGCGATACAAATGAC	2940
Qy	2941	ACATGCCAGATGAGCAAGACTACAGATTCGAATGGCCAAAGTCTTTCGTATAGCCTGGA	3000
Db	2941	ACATGCCAGATGAGCAAGACTACAGATTCGGAATGGCCAAAGTCTTTCGTATAGCCTGGA	3000
Qy	3001	CGGTTTGGTGGNAAACGCATACAGGAGGCTTCTTATCTATCAAGGTGTCACATCTTGA	3060
Db	3001	CGGTTTGGTGGNAAACGCATACAGGAGGCTTCTTATCTATCAAGGTGTCACATCTTGA	3060
Qy	3061	GGCGAAGACCCGGTACTGACTGTACCGCCCAACACAGTCACTCATTTGGGGGCGGAGGC	3120
Db	3061	GGCGAAGACCCAGTACTGACTGTACCGCCCAACACAGTCACTCATTTGGGGGCGGAGGC	3120
Qy	3121	AGAATTTCTCAGATAGGCACTCTCATTTTCTTGTATCAACGAGGTCATCATCTTCTCT	3180
Db	3121	AGAATTTCTCAGATAGGCACTCTCATTTTCTTGTATCAGCGAGGTCATCATCTTCTCT	3180
Qy	3181	CCCGCTTTATATCTTATGACGTACGACCAAAACAGCCACTCTTTCATAGTCTTAT	3240
Db	3181	CCCGCTTTATATCTTATGACGTACGACCAAAACAGCCACTCTTTCATAGTCTTAT	3240

Qy	3241	ACATTCAATGCTTCACTCGGCCAGGTAGTATCCCTTGCCAGGCTTCAGCAAGATGCCCC	3300
Db	3241	ACATTCAATGCTTCACTCGGCCAGGTAGTATCCCTTGCCAGGCTTCAGCAAGATGCCCC	3300
Qy	3301	AACTCGTGTGTACTCGAGTCTATACAGATCCATATCCCTTAATCTTCTATAGAAACC	3358
Db	3301	AACTCGTGTGTACTCGAGTCTATACAGATCCATATCCCTTAATCTTCTATAGAAACC	3358
RESULT 3			
5310678-2			
; Patent No. 5310678			
; APPLICANT: Bingham, Richard W.; Chambers, Philip; Emerson, Peter			
; T.; Millar, Neil S.			
; TITLE OF INVENTION: NEWCASTLE DISEASE VIRUS GENE CLONES			
; NUMBER OF SEQUENCES: 3			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/07/438,945			
; FILING DATE: 17-NOV-1989			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: 885,765			
; FILING DATE: 15-JUL-1986			
; SEQ ID NO:2:			
; LENGTH: 3825			
5310678-2			
Query Match 95.2%; Score 3196.4; DB 6; Length 3825;			
Best Local Similarity 97.0%; Pred. No. 0;			
Matches 3257; Conservative 0; Mismatches 101; Indels 0; Gaps 0;			
Qy	1	ACGGGTAGAAGATTCTGGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGCTCCAGACC	60
Db	1	ACGGGTAGAAGATTCTGGATCCCGGTTGGCGCCCTTCTAGGTGCAAGATGGCGCCAGACC	60
Qy	61	TTCTACCAAGAAACCCAGCACCTATGATGCTGACTATCCGGGTTCCGCTGCGCTGAGTTG	120
Db	61	TTCTACCAAGAACCCAGTACCTATGATGCTGACTGTCGAGTCCGCTGCTGACTGAGTTG	120
Qy	121	CATCTGTCCGGCAAACTCCATTGATGGAGGCGCTCTTGCAAGTCCAGGAATTTGGTTAC	180
Db	121	CATCTGTCCGGCAAACTCCATTGATGGAGGCGCTCTTGCGGCTGCAGGAATTTGGTAAAC	180
Qy	181	AGGAGACAAAGCCGTCAACATATACACTCATCCAGACAGGATCAATCATAGTTAAGCT	240
Db	181	AGGAGACAAAGCGTCAACATATACACTCATCCAGACAGGATCAATCATAGTTAAGCT	240
Qy	241	CCTCCGAAATCGCCCAAGGATAAGGAGGCAATGTGCGAAAGCCCTTTGGATGCATCAA	300
Db	241	CCTCCCAAACTCGCCCAAGGATAAGGAGGCAATGTGCGAAAGCCCTTTGGATGCATCAA	300
Qy	301	CAGACATTTGACCACTTTGCTCAACCCCTTTGGTACTCTATCCGTAGGATACAGAGTC	360
Db	301	CAGACATTTGACCACTTTGCTCAACCCCTTTGGTACTCTATCCGTAGGATACAGAGTC	360
Qy	361	TGTCACTACATCTCGAGGGGGAGACAGGGGCGCTTATAGGCGCCATTTATGGCGGTGT	420
Db	361	TGTAACTACATCTGAGGGGAGACAGAAACGCTTTATAGGCGCCATTTATGGCGGTGT	420
Qy	421	GGCTCTTTGGGTTGCAACTGCGGCACAAATAACAGCGGCGCAGCTCTGATACAAAGCAA	480
Db	421	GGCTCTTTGGGTTGCAACTGCTGCACAAATAACAGCGGCGCAGCTCTGATACAAAGCAA	480
Qy	481	ACAAATGCTGCCAATCTCCGACTTAAAGAGGCAATTTGCCCGCAACCAATGAGGCTGT	540
Db	481	ACAAATGCTGCCAATCTCTCCGACTTAAAGAGGCAATTTGCCCGCAACCAATGAGGCGGT	540
Qy	541	GCATGAGTCACTGACGGAATTTATCCCACTAGCAGTGGCAGTTGGGAAGATGCAAGAGTT	600
Db	541	GCATGAGTCACTGACGGAATTTATCCCACTAGCAGTGGCAGTTGGGAAGATGCAAGAGTT	600
Qy	601	TGTTAATGACCAATTTTAAATAAAACAGCTCAGGAATTAGACTGCATCAAAATTTGCACAGCA	660

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QY 1741 TAATTTGTGCAAGTTCTGTAGTCTGTCTGTCAGTTTACAGAGAGTTAAGAAAAAATCTACCGGT 1800
Db 1741 TAATTTGTGCAAGTTCTGTAGTCTGTCTGTCAGTTTACAGAGAGTTAAGAAAAAATCTACCGGT 1800
QY 1801 TGATAGTGAACAAAGGACGATATACGGGTAGAACGGTAAAGAGAGCGCGCCCTCAATTGC 1860
Db 1801 TGATAGTGAACAAAGGACGATATACGGGTAGAACGGTAAAGAGAGCGCGCCCTCAATTGC 1860
QY 1861 GAGCAGGCTTCAACACTCGTTCTACCGTTACCGCAACAGTCTCTCAATCATGGAC 1920
Db 1861 GAGCAGGCTTCAACACTCGTTCTACCGTTACCGCAACAGTCTCTCAATCATGGAC 1920
QY 1921 CGCGCCGTAGCCAAAGTTGGTTAGAGAAATGATGAAGAGAGGCAAAAAATACATGCGCG 1980
Db 1921 CGCGCAGTTAGCCAAAGTTGGTTAGAGAAATGATGAAGAGAGGCAAAAAATACATGCGCG 1980
QY 1981 TTGATATTCGGATTCGAATCTTATCTTAAACAGTAGTAGTACCTTGGCTATPATCTGTAGCC 2040
Db 1981 TTGATATTCGGATTCGAATCTTATCTTAAACAGTAGTAGTACCTTGGCTATPATCTGTAGCC 2040
QY 2041 TCCTTTTATATAGCATGGGGCTAGCACACCTAGCGATCTTGTAGGCATACCGACTAGG 2100
Db 2041 TCCTTTTATATAGCATGGGGCTAGCACACCTAGCGATCTTGTAGGCATACCGACTAGG 2100
QY 2101 ATTTCCAGGGCAGAGAAAAAGATTACATCTACACCTTGGTTCCCAATCAAGATGTAGTAGAT 2160
Db 2101 ATTTCCAGGGCAGAGAAAAAGATTACATCTACACCTTGGTTCCCAATCAAGATGTAGTAGAT 2160
QY 2161 AGGATATATAAGCAAGTGGCCCTTGAGTCTCCGTGGCATTTGTAATACTGAGACACA 2220
Db 2161 AGGATATATAAGCAAGTGGCCCTTGAGTCTCCGTGGCATTTGTAATACTGAGACACA 2220
QY 2221 ATTATGACCAATTAACATCTCTCTTATCAGATTAATGGAGCTGCAACACAGTGGG 2280
Db 2221 ATTATGACCAATTAACATCTCTCTTATCAGATTAATGGAGCTGCAACACAGTGGG 2280
QY 2281 TGCGGGCAGCTATCCATGACCCAGATTATATAGGGGGGATAGGCAAGAACTCATTTGTA 2340
Db 2281 TGCGGGCAGCTATCCATGACCCAGATTATATAGGGGGGATAGGCAAGAACTCATTTGTA 2340
QY 2341 GATGATGCTAGTGATGTCATCATCTATCCCTCTGTCATTTCAAGAACATCTGAATTTT 2400
Db 2341 GATGATGCTAGTGATGTCATCATCTATCCCTCTGTCATTTCAAGAACATCTGAATTTT 2400
QY 2401 ATCCCGGCGCTACTACAGATCAGGTTGCACTCGAATACCTTCATTTGACATGAGTCT 2460
Db 2401 ATCCCGGCGCTACTACAGATCAGGTTGCACTCGAATACCTTCATTTGACATGAGTCT 2460
QY 2461 ACCCATTTACTGCTACACCCATAATGTAATATTGTCGTGATGCAAGATCACTCACATTCA 2520
Db 2461 ACCCATTTACTGCTACACCCATAATGTAATATTGTCGTGATGCAAGATCACTCACATTCA 2520
QY 2521 TATCAGTATTTAGCATTGGTGTGCTCCGGACATCTGCAACAGGAGGGTATTTCTTTCT 2580
Db 2521 TATCAGTATTTAGCATTGGTGTGCTCCGGACATCTGCAACAGGAGGGTATTTCTTTCT 2580
QY 2581 ACTCTGGGTTCCATCAACCTGGAGGACACCCCAAAATCGGAAGTCTTGCAGTGTAGTGCA 2640
Db 2581 ACTCTGGGTTCCATCAACCTGGAGTGAACAGCAAAATCGGAAGTCTTGCAGTGTAGTGCA 2640
QY 2641 ACTCCCTCGGTTGTGATATGCTGTGCTCGAAAGTCAAGAGACAGAGGAAGAGATTAT 2700
Db 2641 ACTCCCTCGGTTGTGATATGCTGTGCTCGAAAGTCAAGAGACAGAGGAAGAGATTAT 2700
QY 2701 AACTCAGCTCTCCCTACCGGATGGTACATGGGAGGTTAGGGTTGCAAGCGCCAGTACCAC 2760
Db 2701 AACTCAGCTCTCCCTACCGCTGATGGACATGGGAGGTTAGGGTTGCAAGCGCCAGTACCAC 2760
QY 2761 GAAAAGACCTAGATGTCACAAATTTATTCGGGACCTGGGTGGCCAACTACCCAGGAGTA 2820
Db 2761 GAAAAGACCTAGACGTCACAAATTTATTTGAGGACCTGGGTGGCCAACTACCCAGGAGTA 2820
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QY 2821 GGGGGTGGATCTTTTATTGACAGCCCGGTATGGTTCTAGTCTTACGAGGGTTAAAACCC 2880
Db 2821 GGGGGTGGATCTTTTATTGACAGCCCGGTATGGTTCTAGTCTTACGAGGGTTAAAACCC 2880
QY 2881 AATTCAACCCAGTGAACACTGTGTACAGGAAGGAAATATGTATATACAAGCGATACATGAC 2940
Db 2881 AATTCAACCCAGTGAACACTGTGTACAGGAAGGAAATATGTATATACAAGCGATACATGAC 2940
QY 2941 ACATGCCAGATGACGAAGACTACAGATTCCGAATGGCCAAAGTCTTCTGATATAGCCCTGA 3000
Db 2941 ACATGCCAGATGACGAAGACTACAGATTCCGAATGGCCAAAGTCTTCTGATATAGCCCTGA 3000
QY 3001 CGGTTTGGTGGGAAACGCATACAGCAGGCTATCTTATCTATCAAGGTGTCAACATCTTTA 3060
Db 3001 CGGTTTGGTGGGAAACGCATACAGCAGGCTATCTTATCTATCAAGGTGTCAACATCTTTG 3060
QY 3061 GCGGAAGACCCGGTACTGTGTACCGCCCAACAGTCACTCATGTGGGGCCGGAAGGC 3120
Db 3061 GCGGAAGACCCGGTACTGTGTACCGCCCAACAGTCACTCATGTGGGGCCGGAAGGC 3120
QY 3121 AGAATTTCTCACAGTAGGGACATCTCAATTTCTTGTATCAGGAGGTCATCATCTTCTCT 3180
Db 3121 AGAATTTCTCACAGTAGGGACATCTCAATTTCTTGTATCAGGAGGTCATCATCTTCTCT 3180
QY 3181 CCGCGCTTATTATATCTTATGACAGTCAGCAACAAACAGCCACTCTTCTATAGTCTCTTAT 3240
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QY 3241 ACATTTCAATGCTTCACTCGCCAGGATGATTCCTTGGCAGGCTTTCAGCAAGATGCCCC 3300
Db 3241 ACATTTCAATGCTTCACTCGCCAGGATGATTCCTTGGCAGGCTTTCAGCAAGATGCCCC 3300
QY 3301 AACTCGTGTGTACTCGAGTCTATACAGATCCATATCCCTAATCTTCTATAGAAACC 3358
Db 3301 AACTCGTGTGTACTCGAGTCTATACAGATCCATATCCCTAATCTTCTATAGAAACC 3358
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RESULT 4

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US-08-484-575A-12
; Sequence 12, Application US/08484575A
; Patent No. 5925358
; GENERAL INFORMATION:
; APPLICANT: Mark D. Cochran and David E. Junker
; TITLE OF INVENTION: Recombinant Fowlpox Viruses and Uses Thereof
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,575A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq, John P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)278-0450
; TELEFAX: (212)391-0525
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4177 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
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HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE: CDS
NAME/KEY: CDS
LOCATION: 115..1860
FEATURE: CDS
NAME/KEY: CDS
LOCATION: 2095..3756
US-08-484-575A-12

Query Match
Best Local Similarity 51.9%; Score 1741.8; DB 2; Length 4177;
Matches 1755; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

Qy 16 TGGATCCCGGTGGCGCCCTCCAGGTGCAAGATGGGTCCAGACTCTTCTACCAAGAACC 75
Db TCGATCCCGGTGGCGCCCTCCAGGTGCAAGATGGGTCCAGACTCTTCTACCAAGAACC 2123

Qy 76 AGCACCTATGATGCTGACTATCCGGGTGGCGCTGGCACTGATGTCATCTGTCGGCAAA 135
Db AGCACCTATGATGCTGACTATCCGGGTGGCGCTGGCACTGATGTCATCTGTCGGCAAA 2183

Qy 136 CTCGATTTGATGGCAGGCTCTTTCAGCTGACAGGAAATGTTGTTACAGAGACAAAGCCGT 195
Db CTCGATTTGATGGCAGGCTCTTTCAGCTGACAGGAAATGTTGTTACAGAGACAAAGCAGT 2243

Qy 196 CAACATATACACCTCATCCAGACAGGATCAATCATAGTTAAGTCTCTCCCGATCTGCC 255
Db CAACATATACACCTCATCCAGACAGGATCAATCATAGTTAAGTCTCTCCCGATCTGCC 2303

Qy 256 CAAGGATAAGAGGATGTTGGAAAGCCCTTGGATGCTATCAACAGGACATTTGACCAC 315
Db AAAGGATAAGAGGATGTTGGAAAGCCCTTGGATGCTATCAACAGGACATTTGACCAC 2363

Qy 316 TTTGCTCACCCCTTGGTGAATCTATCCGTAGGATCAAGAGTCTGTGACTACATCTGG 375
Db TTTGCTCACCCCTTGGTGAATCTATCCGTAGGATCAAGAGTCTGTGACTACATCTGG 2423

Qy 376 AGGGGGAGACAGGGGGCCCTTATAGCGCCATTTATGGCGGTGGCTCTTGGGGTGC 435
Db AGGGGGAGACAGGGGGCCCTTATAGCGCCATTTATGGCGGTGGCTCTTGGGGTGC 2483

Qy 436 AACTGCCGCAAAATAACAGGGCGGAGCTCTGATACAGGCCAAACAAATGCTGCCAA 495
Db AACTGCCGCAAAATAACAGGGCGGAGCTCTGATACAGGCCAAACAAATGCTGCCAA 2543

Qy 496 CATCCTCGACTTAAGAGAGCATTTGGCAACCAATGAGGCTGTGATGAGGTCACTGA 555
Db CATCCTCGACTTAAGAGAGCATTTGGCAACCAATGAGGCTGTGATGAGGTCACTGA 2603

Qy 556 CGGATTATCGCAACTAGCAGTGGCAGTTTGGGAAGATGACAGATTTGTTAATGACCAATT 615
Db CGGATTATCGCAACTAGCAGTGGCAGTTTGGGAAGATGACAGATTTGTTAATGACCAATT 2663

Qy 616 TAATAAACAGCTCAGGAATPAGACTGATCAAAATTTGCAAGCAAGTTGGTGTAGAGCT 675
Db TAATAAACAGCTCAGGAATPAGACTGATCAAAATTTGCAAGCAAGTTGGTGTAGAGCT 2723

Qy 676 CAACCTGTACTAACCGAATTTGATACAGTATTCGGACCAACATCACTTCCAGCTGTT 735
Db CAACCTGTACTAACCGAATTTGATACAGTATTCGGACCAACATCACTTCCAGCTGTT 2783

Qy 736 AAACAAGCTGACTATTACAGGACATTTTCAATCTAGCTGGTGGAAATATGGATTACTTAT 795
Db AAACAAGCTGACTATTACAGGACATTTTCAATCTAGCTGGTGGAAATATGGATTACTTAT 2843

Qy 796 GACTAAGTTAGGTGTAGGGAACAATCAACTCAGCTCAATTAATCGGTAGCGGTAAATCAC 855
Db GACTAAGTTAGGTGTAGGGAACAATCAACTCAGCTCAATTAATCGGTAGCGGTAAATCAC 2903

Qy 856 CGGTAAACCTATTCTATACGACTCACAGATCACTCTTGGGTATACAGTTAATCTTACC 915
Db CGGTAAACCTATTCTATACGACTCACAGATCACTCTTGGGTATACAGTTAATCTTACC 2963

RESULT 5

US-08-477-459-12

; Sequence 12, Application US/08477459

; Patent No. 6001369

; GENERAL INFORMATION:

; APPLICANT: Mark D. Cochran

; TITLE OF INVENTION: Recombinant Fowlpox Viruses and Uses

; TITLE OF INVENTION: Thereof

; NUMBER OF SEQUENCES: 20

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: John P. White

Qy 916 TTCAGTCGGGAACCTAAATAATATGCGTGCACCTACTTGGAAAACCTTATCCGTAAGCAC 975
Db TTCAGTCGGGAACCTAAATAATATGCGTGCACCTACTTGGAAAACCTTATCCGTAAGCAC 3023

Qy 976 AACAGGGGATTTGCTTCGGCACCTTGTCCCAAAGTGGTGACACAGGTCCGTTCTGTGAT 1035
Db AACAGGGGATTTGCTTCGGCACCTTGTCCCAAAGTGGTGACACAGGTCCGTTCTGTGAT 3083

Qy 1036 AGAAGAACTTGACACCTCATATGTTATAGAACTGACTTAGATTATATTTGTACAAGAA 1095
Db AGAAGAACTTGACACCTCATATGTTATAGAACTGACTTAGATTATATTTGTACAAGAA 3143

Qy 1096 AGTAAAGTTCCTATATGTCCTCCCTGGTATTTATCTGCTTTCAGCGGCAATACGTCGGCTG 1155
Db AGTAAAGTTCCTATATGTCCTCCCTGGTATTTATCTGCTTTCAGCGGCAATACATCGGCTG 3203

Qy 1156 TATGTACTCAAGACCGAAGCGCATTACTACACCATATCATGACTATCAAAAGGTTTCAGT 1215
Db TATGTACTCAAGACCGAAGCGCATTACTACACCATATCATGACTATCAAAAGGTTTCAGT 3263

Qy 1216 CATCGCAACTGCAAGATGACAAATGTAGATGTGTAACCCCGGGGTATCATATCGCA 1275
Db CATCGCAACTGCAAGATGACAAATGTAGATGTGTAACCCCGGGGTATCATATCGCA 3323

Qy 1276 AACTATGGAAGACCGGTCTCTTAATAGATAAACAATCATGCAATGTTTTATCCTTAGG 1335
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; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,459
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq, John P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4177 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 115..1860
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2095..3756
; US-08-477-459-12

Query Match 51.9%; Score 1741.8; DB 3; Length 4177;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1755; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

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RESULT 6
US-08-479-869-12
; Sequence 12, Application US/08479869
; Patent No. 6123949
; GENERAL INFORMATION:
; APPLICANT: Cochran Ph.D, Mark D
; TITLE OF INVENTION: Recombinant Fowlpox Virus S-PPV-043 and
; TITLE OF INVENTION: Uses Thereof
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,869
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/024,156
; FILING DATE: 26-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq, John P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)977-9550
; TELEFAX: (212)664-0525
; TELEX: 422523
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4177 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 115..1860
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2095..3756
US-08-479-869-12

Query Match 51.9%; Score 1741.8; DB 3; Length 4177;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1755; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

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Db 2064 TCGATCCCGGTTGGCGCCCTCCAGGTCGAAGATGGGCTCCAGACCTTCTACCAAGAACCC 2123

Qy 76 AGACCTTATGATGCTGACTATCCGGTTGCGCTGGCACTGAGTTGCTGTCGGCAAA 135
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Qy 1696 TACAAAATGTGACACAGATGAGGAAGAGGTTTCCCTAATAGTAATTTGTGTGAAG 1755
Db 3744 TACAAAATGTGACACAGATGAGGAAGAGGTTTCCCTAATAGTAATTTGTGTGAAG 3803
Qy 1756 TTCTGCTAGTCTGTCAGTTCAGAGAGTTTAAAGAAAAA 1792
Db 3804 TTCTGCTAGTCTGTCAGTTCAGAGAGTTTAAAGAAAAA 3840
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RESULT 8

PCT-US94-01826A-12

; Sequence 12, Application PC/TUS9401826A

; GENERAL INFORMATION:

; APPLICANT: Syntro Corporation, et al.

; TITLE OF INVENTION: Recombinant Fowlpox Virus S-FPV-043 and Uses Thereof

; NUMBER OF SEQUENCES: 20

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: John P. White

; STREET: 30 Rockefeller Plaza

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10112

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US94/01826A

; FILING DATE: 28-FEB-1994

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

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;

;

;

```
; NAME: White Esq. John P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)977-9550
; TELEFAX: (212)664-0525
; TELEX: 422523
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4177 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 115..1860
; NAME/KEY: CDS
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2095..3756
; PCT-US94-01826A-12
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Query Match 51.9%; Score 1741.8; DB 5; Length 4177;

Best Local Similarity 98.8%; Pred. No. 0;

Matches 1755; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

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Qy 16 TGGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACCTTTTACCAAGAACCC 75
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1696 TACAAAAATGTGAACACAGATAGGAACGAAGGTTTCCCTAATAGTAATTTGTGAAAG 1755
DB TACAAAAATGTGAACACAGATAGGAACGAAGGTTTCCCTAATAGTAATTTGTGAAAG 3803
1756 TTCTGTAGTCTGTGAGTTTCAGAGAGTTAAGAAAAA 1792
DB TTCTGTAGTCTGTGAGTTTCAGAGAGTTAAGAAAAA 3840

RESULT 9
PCT-US94-02252A-12
; Sequence 12, Application PC/TUS9402252A
; GENERAL INFORMATION:
; APPLICANT: Syntro Corporation, et al.
; TITLE OF INVENTION: Recombinant Fowlpox Viruses and Uses Thereof
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/02252A
; FILING DATE: 28-FEB-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq, John P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)977-9550
; TELEFAX: (212)664-0525
; TELEX: 422523
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4177 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 115..1860
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2095..3756
; PCT-US94-02252A-12
Query Match 51.9%; Score 1741.8; DB 5; Length 4177;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1755; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
QY 16 TGGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACCTTCTACCAAGAACCC 75
DB 2064 TCGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACCTTCTACCAAGAACCC 2123
QY 76 AGCACCTATGATGCTGACTATCCGGGTTCGGCTGGCACTGAGTTGCACTGTCCGGCAAA 135
DB 2124 AGCACCTATGATGCTGACTATCCGGGTTCGGCTGGCACTGAGTTGCACTGTCCGGCAAA 2183
QY 136 CTCCTATTGATGGAGGCTCTTTCAGCTCGAGGAATTTGGTTACAGGAGACAAAGCCGT 195
DB 2184 CTCCTATTGATGGAGGCTCTTTCAGCTCGAGGAATTTGGTTACAGGAGACAAAGCAGT 2243
QY 196 CAACATATACCTCATCCAGACAGGATCAATAGTTAAGTCTCTCCCAATCTGCC 255
DB 2244 CAACATATACCTCATCCAGACAGGATCAATAGTTAAGTCTCTCCCAATCTGCC 2303
QY 256 CAAGGATAAGGAGGATGTGCGAAAGCCCTTTGGATGCATACAAAGGACATTGACCAC 315
DB 2304 AAAGGATAAGGAGGATGTGCGAAAGCCCTTTGGATGCATACAAAGGACATTGACCAC 2363
QY 316 TTTGCTCAACCCCTTTGGTGTACTCTATCCGTAGGATACAGAGTCTGTGACTACATCTGG 375

2364	Db	TTTGGTCACCCCCCTTGGTGACTCTATCCGTAAGGATCAAGAGTCTCTGTGACTACATCATCGG	2422
376	Qy	AGGGGGAGACAGGGGGCCCTTATAGCGCCATTATTGGCGGCTGTGCTCTTGGGGTTGC	435
2424	Db	AGGGGGAGACAGGGGGCCCTTATAGGGCCATTATTGGCGGTGGCTCTTGGGGTTGC	2483
436	Qy	AATGCGCGCAAAATAACAGCGCGCGCAGCTCTGATACAAGCCMAACAAAATGCTGCA	495
2484	Db	AATGCGCGCAAAATAACAGCGCGCGCAGCTCTGATACAAGCCMAACAAAATGCTGCA	2543
496	Qy	CATCCTCCGACTTAAAGAGAGCATTTGCGCAACCAATGAGCGCTGTCATCAGAGTCACTGA	555
2544	Db	CATCCTCCGACTTAAAGAGAGCATTTGCGCAACCAATGAGCGCTGTCATCAGAGTCACTGA	2603
556	Qy	CGGATTATCGCAATAGCAGTGGCAGTTGGGAAGATCAGCAGTTTCTTAATGACCAATT	615
2604	Db	CGGATTATCGCAATAGCAGTGGCAGTTGGGAAGATCAGCAGTTTCTTAATGACCAATT	2663
616	Qy	TAATAAAACAGCTCAGGAATTAGACTGTCATCAAAATTGCAACGAAGTTGGTGTGAGCT	675
2664	Db	TAATAAAACAGCTCAGGAATTAGACTGTCATCAAAATTGCAACGAAGTTGGTGTGAGCT	2723
676	Qy	CAACCTGTACTTAACCGAATTGACTACAGTATTCGGACCACAATCACTTCACTGCTTT	735
2724	Db	CAACCTGTACTTAACCGAATTGACTACAGTATTCGGACCACAATCACTTCACTGCTTT	2783
736	Qy	AAACAAGCTGACTATTCAAGGCACCTTTACAATCTAGCTGGTGGAAATGAGTACTTTATT	795
2784	Db	AAACAAGCTGACTATTCAAGGCACCTTTACAATCTAGCTGGTGGAAATGAGTACTTTATT	2843
796	Qy	GACTAAGTTAGGTAGGGAACAATCAACTCAGCTCAATTAATCGGTAGCGGCTTAATCAC	855
2844	Db	GACTAAGTTAGGTAGGGAACAATCAACTCAGCTCAATTAATCGGTAGCGGCTTAATCAC	2903
856	Qy	CGGTAAACCCCTATTCTATACGACTCAGACTCAACTCTTGGGTATACAGGTAATCTTACC	915
2904	Db	CGGTAAACCCCTATTCTATACGACTCAGACTCAACTCTTGGGTATACAGGTAATCTTACC	2963
916	Qy	TTCACTCGGGAACTTAAATAATATGCGTGCCACTTCTTGGAAACCTTTATCCGTGAAGCAC	975
2964	Db	TTCACTCGGGAACTTAAATAATATGCGTGCCACTTCTTGGAAACCTTTATCCGTGAAGCAC	3023
976	Qy	AACACAGGGGATTTGCCCTCGGCACCTTGTCCAAAGAGTGGTGACACAGGTCGGTTCTGTGAT	1035
3024	Db	AACACAGGGGATTTGCCCTCGGCACCTTGTCCAAAGAGTGGTGACACAGGTCGGTTCTGTGAT	3083
1036	Qy	AGAAGAACTTGACACCTCATACTGTATAGAACTGACTTAGATTATATTTGTAACAAGAT	1095
3084	Db	AGAAGAACTTGACACCTCATACTGTATAGAACTGACTTAGATTATATTTGTAACAAGAT	3143
1096	Qy	AGTAAACGTTCCCTATGTCCCTGGTATTTATTTCTGCTTGAGCGGCAATACGTCGGCGTG	1155
3144	Db	AGTAAACGTTCCCTATGTCCCTGGTATTTATTTCTGCTTGAGCGGCAATACGTCGGCGTG	3203
1156	Qy	TATGTACTCAAGAAGCGGACCTTACTTACCAATACATGACTATCAAGGTTTCAGT	1215
3204	Db	TATGTACTCAAGAAGCGGACCTTACTTACCAATACATGACTATCAAGGTTTCAGT	3263
1216	Qy	CATCGGCAACTGCAAGATGACAAATGTAGATGTGTAACCCCGGGTATCATATGCGA	1275
3264	Db	CATCGGCAACTGCAAGATGACAAATGTAGATGTGTAACCCCGGGTATCATATGCGA	3323
1276	Qy	AAACTATGGAGAGCCGTGTCTCTAAATAGATTAACAAATCATGCAATGTTTTATTCCTTAGG	1335
3324	Db	AAACTATGGAGAGCCGTGTCTCTCTAAATAGATTAACAAATCATGCAATGTTTTATTCCTTAGG	3383
1336	Qy	CGGGATAACTTTTAAGGCTCAGTGGGGAATTCGATGTAACTTTATCAGAAGAAATATCTCAAT	1395
3384	Db	CGGGATAACTTTTAAGGCTCAGTGGGGAATTCGATGTAACTTTATCAGAAGAAATATCTCAAT	3443
1396	Qy	ACAAGATTCTCAAGTAATAATAACAGGCAATCTTGATATCTCAACTGAGCTTGGGAATGT	1455
3444	Db	ACAAGATTCTCAAGTAATAATAACAGGCAATCTTGATATCTCAACTGAGCTTGGGAATGT	3503

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RESULT 10
US-08-663-566A-12
; Sequence 12, Application US/08663566A
; Patent No. 5853733
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D
; APPLICANT: Macdonald, Richard D
; TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys
; TITLE OF INVENTION: and Uses Thereof
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/663,566A
; FILING DATE: June 13, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; REGISTRATION NUMBER: 28,678
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)278-0400
; TELEFAX: (212)391-0526
; TELEX: 422523
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1662 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; .NAME/KEY: CDS
; .LOCATION: 1..1662
US-08-663-566A-12

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Query Match		48.6%; Score 1631.6; DB 2; Length 1662;
Best Local Similarity		98.9%; Pred. No. 0;
Matches 1643; Conservative		0; Mismatches 19; Indels 0; Gaps 0;
QY	47	ATGGGCTCAGAGCTTCTACCAAGAACCCAGCACTTATGATGCTGACTATCCGGGTGGC 106
DB	1	ATGGGCTCAGAGCTTCTACCAAGAACCCAGCACTTATGATGCTGACTATCCGGGTGGC 60
QY	107	CTGGCACTGAGTTGCTCTGTCGGGCAAACTCCATTGATGGCAGGCTCTTGCACTGCA 166
DB	61	CTGGTACTGAGTTGCTCTGTCGGGCAAACTCCATTGATGGCAGGCTCTTGCACTGCA 120
QY	167	GGAAATTGTGTTACAGAGACAAGCGCTCAACATATACACCTCATCCACAGACAGGATCA 226
DB	121	GGAAATTGTGTTACAGAGACAAGCAGTCAACATATACACCTCATCCACAGACAGGATCA 180
QY	227	ATCATAGTTAAGCTCTCTCCGAATCTGCCAAGGATAAGAGGAGCATGTGGGAAAGCCCC 286
DB	181	ATCATAGTTAAGCTCTCTCCGAATCTGCCAAGGATAAGAGGAGCATGTGGGAAAGCCCC 240
QY	287	TTGGATGCTACACAGGACATTTGACCACTTTGCTCACCCCCCTTGGTGACTCTATCCGT 346
DB	241	TTGGATGCTACACAGGACATTTGACCACTTTGCTCACCCCCCTTGGTGACTCTATCCGT 300
QY	347	AGGATACAAGAGTCTGTGACTACATCTGGAGGGGGAGACAGGGGGCCCTTATAGGCGCC 406
DB	301	AGGATACAAGAGTCTGTGACTACATCTGGAGGGGGAGACAGGGGGCCCTTATAGGCGCC 360
QY	407	ATTATTGGGGTGTGCTCTTGGGTTGCACTTGGCGCAAAATAACAGCGGCGGAGCT 466
DB	361	ATTATTGGGGTGTGCTCTTGGGTTGCACTTGGCGCAAAATAACAGCGGCGGAGCT 420
QY	467	CTGATACAGCCAAAACAAATGCTGCCAATCTCTCGACTTAAGAGAGCATTGGCGCA 526
DB	421	CTGATACAGCCAAAACAAATGCTGCCAATCTCTCGACTTAAGAGAGCATTGGCGCA 480
QY	527	ACCAATGAGGCTGTGATGAGGTCACCTGACGGATTATCGCACTAGCAGTGGCAGTTGGG 586
DB	481	ACCAATGAGGCTGTGATGAGGTCACCTGACGGATTATCGCACTAGCAGTGGCAGTTGGG 540
QY	587	AGATGAGCAGTTTGTAAATGACCAATTTAATAAAGCCTCAGGAAATAGACTGCATC 646
DB	541	AGATGAGCAGTTTGTAAATGACCAATTTAATAAAGCCTCAGGAAATAGACTGCATC 600
QY	647	AAATTTGCACAGCAAGTTGGTGTAGAGCTCAACTGTACCTACCGAATTTGACTACAGTA 706
DB	601	AAATTTGCACAGCAAGTTGGTGTAGAGCTCAACTGTACCTACCGAATTTGACTACAGTA 660
QY	707	TTCCGACCAAAATCACTTCCACTGCTTTAAACAAAGCTGACTATTAGGCACTTTACAAT 766
DB	661	TTCCGACCAAAATCACTTCCACTGCTTTAAACAAAGCTGACTATTAGGCACTTTACAAT 720
QY	767	CTAGCTGGTGGAAATATGGATTACTTATTAAGTTAGGTAGGTAGGGAACAATCAACTC 826
DB	721	CTAGCTGGTGGGAATATGGATTACTTATTAAGTTAGGTAGGTAGGGAACAATCAACTC 780
QY	827	AGCTCATTATCGGTAGCGCTTAATCACCGGTAAACCTATTCTATACGACTCACAGACT 886
DB	781	AGCTCATTATCGGTAGCGCTTAATCACCGGTAAACCTATTCTATACGACTCACAGACT 840
QY	887	CAACTCTTGGGTATACAGGTAACTCTACCTTCACTGGGAACTTAATATATGCGTGGC 946
DB	841	CAACTCTTGGGTATACAGGTAACTCTACCTTCACTGGGAACTTAATATATGCGTGGC 900
QY	947	ACTACTTGGAAACCTTTATCGTAAGCAACACAGGGGATTTGCCCTGGCACTTGCCCA 1006
DB	901	ACTACTTGGAAACCTTTATCGTAAGCAACACAGGGGATTTGCCCTGGCACTTGCCCA 960
QY	1007	AAAGTGTGACAGGTCGGTCTGTGATAGAGACTTGACACCTCATCTATAGTA 1066
DB	961	AAAGTGTGACAGGTCGGTCTGTGATAGAGACTTGACACCTCATCTATAGTA 1020
QY	1067	ACTGACTTAGATTATTTGTAACAAGAAATAGTAACGTTCCCTATGTCCTCGTATTAT 1126

DB	1021	ACTGACTTAGATTATTTATTTGTAACAATAAGTAACGTTCCCTATGTCCTCGTATTATAC 1080
QY	1127	TCTGCTTTCAGCGGCAATACGTCGGCTCTGATGCTACTCAAGACCGAAGCGCACCTACT 1186
DB	1081	TCTGCTTTCAGCGGCAATACATCGGCTCTGATGCTACTCAAGACCGAAGCGCACCTACT 1140
QY	1187	ACACCATACATGACTATCAAGGTTCAAGTCATCGCCAACTGCAAGATGACCAATGTAGA 1246
DB	1141	ACACCATATATGACTATCAAGGCTCAGTCATCGCTAACTGCAAGATGACCAATGTAGA 1200
QY	1247	TGTGTAAAACCCCGGGTATCATATCGAAAACTATGGAAGACCCGTGCTCTTAATAGAT 1306
DB	1201	TGTGTAAAACCCCGGGTATCATATCGAAAACTATGGAAGACCCGTGCTCTTAATAGAT 1260
QY	1307	AAACATCATGCAATGTTTTATCTTCTAGGGGGGATAAATTAAAGGCTCAGTGGGGAATTC 1366
DB	1261	AAACATCATGCAATGTTTTATCTTCTAGGGGGGATAAATTAAAGGCTCAGTGGGGAATTC 1320
QY	1367	GATGTAACCTTATCAGAAAGATATCTCAATAACAAGATTCTCAAGTAATAAACAAGCAAT 1426
DB	1321	GATGTAACCTTATCAGAAAGATATCTCAATAACAAGATTCTCAAGTAATAAACAAGCAAT 1380
QY	1427	CTTGATATCTCAACTGAGCTTGGGAATGTCAACAACCTCGATCAGTAATGCTTTGAATAAG 1486
DB	1381	CTTGATATCTCAACTGAGCTTGGGAATGTCAACAACCTCGATCAGTAATGCTTTGAATAAG 1440
QY	1487	TTAGAGGAAGCAACAGAAACTAGACAAGTCAATGTCAAACTGACTAGCACATCTGCT 1546
DB	1441	TTAGAGGAAGCAACAGAAACTAGACAAGTCAATGTCAAACTGACTAGCACATCTGCT 1500
QY	1547	CTCATTACCTATATCGTTTGTACTATCATCTCTTTGTTTGGTATATCTTAGCCTGATT 1606
DB	1501	CTCATTACCTATATCGTTTGTACTATCATCTCTTTGTTTGGTATATCTTAGCCTGATT 1560
QY	1607	CTAGCATGTCTAATGTACAAGCAAAAGGCGCAACAAAAACCTTATATGGCTTGGG 1666
DB	1561	CTAGCATGTCTAATGTACAAGCAAAAGGCGCAACAAAAACCTTATATGGCTTGGG 1620
QY	1667	ATAATATCTTAGATCAGATGAGGCCACTACAAAAATGTGA 1708
DB	1621	ATAATATCTTAGATCAGATGAGGCCACTACAAAAATGTGA 1662

RESULT 11
US-08-023-610-12
; Sequence 12, Application US/08023610
; Patent No. 5928648
; GENERAL INFORMATION:
; APPLICANT: Cochran Ph.D, Mark D
; APPLICANT: Macdonald Ph.D, Richard D
; TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys
; TITLE OF INVENTION: and Uses Thereof
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/023.610
; FILING DATE: February 26, 1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq, John P
; TELECOMMUNICATION INFORMATION:

:	TELEPHONE:	(212)977-9550
:	TELEFAX:	(212)664-0525
:	TELEX:	422523
:	INFORMATION FOR SEQ ID NO:	12:
:	SEQUENCE CHARACTERISTICS:	
:	LENGTH:	1662 base pairs
:	TYPE:	nucleic acid
:	STRANDEDNESS:	double
:	TOPOLOGY:	linear
:	MOLECULE TYPE:	DNA (genomic)
:	HYPOTHETICAL:	NO
:	ANTI-SENSE:	NO
:	FEATURE:	
:	NAME/KEY:	CDS
:	LOCATION:	1..1662
:	US-08-023-	610-12

Query Match

Best Local Similarity

Matches 1643; Conservative

48.6%;

98.9%;

0;

Score 1631.6;

Pred. No. 0;

Mismatches 19;

DB 2;

Indels 0;

Gaps 0

Qy	47	ATGGGCTCCAGACCTTCTTACAAGAACCAGAACCTATGATGCTGACTATCGGGTTGGC	106
Db	1	ATGGGCTCCAGACCTTCTTACAAGAACCAGAACCTATGATGCTGACTATCGGGTCGCC	60
Qy	107	CTGCACGTGAGTTCGATCTGTGCCGCAACTCCATTGATGGCAGGCCCTTTGCAGCTGCA	166
Db	61	CTGGTA CTGAGTTGTCATCTGTCCGGCAAACCTCCA TTGATGGCAGGCCCTTTGCAGCTGCA	120
Qy	167	GGAA TTTGGTTACAGGAGACAAAGCCGCTCAACCATATATACACTCATCCAGACAGGATCA	226
Db	121	GGAA TTTGGTTACAGNGACAAGCAGTCAACATATATACACTCATCCAGNACGATCA	180
Qy	227	ATCATATTTAAGCTCTCTCCC GAATCTTGCCCAAGGATAAGGAGGCATGTGCGAAA GCCCCC	286
Db	181	ATCATAGTTAAGCTCTCTCCC GAATCTTGCCAAAGGATAAGGAGGCATGTGCGAAA GCCCCC	240
Qy	287	TTGGATGCATACACAGACCAATTGACCACATTTTGCTCACCCCCCTTGGTGACTCTATCCGT	346
Db	241	TTGGATGCATACAA CAGACCAATTGACCACATTTTGCTCACCCCCCTTGGTGACTCTATCCGT	300
Qy	347	AGGATACAAGAGTCTGTGACTTACATCTGGAGGGGGGAGACAGGGCGCCTTTATAGCGGCC	406
Db	301	AGGATACAAGAGTCTGTGACTTACATCTGGAGGGGGGAGACAGGGCGCCTTTATAGCGGCC	360
Qy	407	ATTATTTGGCGGTGTGGCTCTTTGGGGTTGCAACTGCGCGCACAAATAA CAGCGCCGACGT	466
Db	361	ATTATTTGGCGGTGTGGCTCTTTGGGGTTGCAACTGCGCGCACAAATAA CAGCGCCGACGT	420
Qy	467	CTGATACAAGCCAAACAAAAATGCTGCCAAACCTCTCCGACTTAAAGAGAGGATTTCCCGCA	526
Db	421	CTGATACAAGCCAAACAAAAATGCTGCCAAACCTCTCCGACTTAAAGAGAGGATTTCCCGCA	480
Qy	527	ACCAATGAGGCTGTGCTAGGTCAC TGA CGGAATTCGCAACTAGCAGTGGCAGTTGGG	586
Db	481	ACCAATGAGGCTGTGCTAGGTCAC TGA CGGAATTCGCAACTAGCAGTGGCAGTTGGG	540
Qy	587	AAGATGACGAGTTTGGTTAATGACCAATTTAATAAA CAGCTCAGGAATTAGACTGCATC	646
Db	541	AAGATGACGAGTTTGGTTAATGACCAATTTAATAAA CAGCTCAGGAATTAGACTGCATC	600
Qy	647	AAAATTGCACAGCAAGTTGGTG TAGAGCTCAACCTGTACTTAA CCGAATTGACTACAGTA	706
Db	601	AAAATTGCACAGCAAGTTGGTG TAGAGCTCAACCTGTACTTAA CCGAATTGACTACAGTA	660
Qy	707	TTCGGACCAAAAATCATTCTACCTGCTTTAAACAGCTGACTATTTCAGGCACTTTTACAAT	766
Db	661	TTCGGACCAAAAATCATTCTACCTGCTTTAAACAGCTGACTATTTCAGGCACTTTTACAAT	720
Qy	767	CTAGCTGGTGGAAATATGGATTACTTATTTGACTAAGTTAGGTGTAGGGAA CAATCAACTC	826
Db	721	CTAGCTGGTGGAAATATGGATTACTTATTTGACTAAGTTAGGTGTAGGGAA CAATCAACTC	780

RESULT 12

RESOLUTION 12
US-08-288-065A-12

US-08-288-005A-12
; Sequence 12, Application US/08288065A

; Patent No. 5961982

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APPLICANT: Cochran, Mark D

APPLICANT: Macdonald, Richard D

TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys S-

TITLE OF INVENTION: HVT-050 and Uses Thereof

NUMBER OF SEQUENCES: 56

CORRESPONDENCE ADDRESS:

ADDRESSEE: John P. White

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/ STREET: 1185 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 10036
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/
/ CURRENT APPLICATION DATA:
/ FILING DATE: Aug-09-94
/ APPLICATION NUMBER: US/08/288,065A
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: White, John P
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212)278-0400
/ TELEFAX: (212)391-0526
/ TELEX: 422523
/
/ INFORMATION FOR SEQ ID NO: 12:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1662 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 1..1662
/
/ US-08-288-065A-12
/
/ Query Match 48.6%; Score 1631.6; DB 2; Length 1662;
/ Best Local Similarity 98.9%; Pred. No. 0;
/ Matches 1643; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
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Db 1621 AATAATACCCTAGATCAGATGAGAGCCACTACAAAATGTGA 1662

RESULT 13

US-08-362-240A-12
; Sequence 12, Application US/08362240A
; Patent No. 5965138
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D
; APPLICANT: Junker, David
; APPLICANT: Wild, Martha A
; TITLE OF INVENTION: Recombinant Herpesvirus and Uses Thereof
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/362,240A
; FILING DATE: Dec-22-94
; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; REGISTRATION NUMBER: 28,678
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)278-0400
; TELEFAX: (212)391-0526
; TELEX: 422523
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1662 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1662
; US-08-362-240A-12

Query Match 48.6%; Score 1631.6; DB 2; Length 1662;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 1643; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 47 ATGGGCTCCAGACCTTCTACCAAGAACCCAGCACCTATGATGCTGACTATCCGGGTTGCG 106
Db 1 ATGGGCTCCAGACCTTCTACCAAGAACCCAGCACCTATGATGCTGACTATCCGGGTTGCG 60
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Db 1621 AATAAATCTCTAGATCAGATGAGAGCCACTACAAAATGTGA 1662

RESULT 14

US-08-804-372A-10
; Sequence 10, Application US/08804372A
; Patent No. 6183753
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D.
; APPLICANT: Wild, Martha A.
; APPLICANT: Winslow, Barbara J.
; TITLE OF INVENTION: Recombinant Chimeric Viruses and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/804,372A
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 2552/39115E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1662 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1662
; US-08-804-372A-10

Query Match 48.6%; Score 1631.6; DB 3; Length 1662;
Best Local Similarity 98.9%; Pred. No. 0;

Matches 1643; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 47 ATGGGCTCCAGACCTTTACTACCAAGAACCCAGACACCTATGATGCTGACTATCCGGGTTCGG 106
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QY 1427 CTTGATATCTCAACTGAGCTTGGGAATGTCAACAACCTCGATCAGTAATGCTTTGAATAAG 1486
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Db 1621 AATAAATCTCTAGATCAGATGAGAGCCACTACAAAAATGTGA 1662

RESULT 15

PCT-US95-10245-12

Sequence 12, Application PC/TUS9510245

GENERAL INFORMATION:

APPLICANT: SYNTRO CORPORATION

TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys And Uses Thereof

NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:

ADDRESSEE: John P. White

STREET: 1185 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/10245

FILING DATE: 09-AUG-1995

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: White, John P

REGISTRATION NUMBER: 28,678

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)278-0400

TELEFAX: (212)391-0526

TELEX: 422523

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:
LENGTH: 1662 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1662
PCT-US95-10245-12

Query Match 48.6%; Score 1631.6; DB 5; Length 1662;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 1643; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

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Job time : 545 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Run on: October 1, 2005, 11:21:58 ; Search time 2138 Seconds
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Gapop 10.0 , Gapext 1.0
Searched: 7442561 seqs, 3452328358 residues

Total number of hits satisfying chosen parameters: 14885122

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Database : Published Applications NA:*

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- 25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	3353.2	99.9	15186	10	US-09-741-744A-134
3	3353.2	99.9	15186	16	US-10-377-718-3
4	3353.2	99.9	15186	17	US-10-429-735-3
5	3353.2	99.9	15186	20	US-10-824-782-134
6	3353.2	99.9	15186	20	US-10-788-232-134
7	3346.8	99.7	15900	17	US-10-440-419-55

8	3198	95.2	15882	17	US-10-440-419-56	Sequence 56, Appl
9	1701.6	50.7	3570	9	US-09-881-457A-1	Sequence 1, Appli
10	1701.6	50.7	3570	24	US-11-126-465-1	Sequence 1, Appli
11	1434.4	42.7	1734	21	US-10-838-834-19	Sequence 19, Appl
12	1414	42.1	1662	19	US-10-725-841-1	Sequence 1, Appli
13	1414	42.1	1662	21	US-10-990-204-1	Sequence 1, Appli
14	1362.8	40.6	1662	9	US-09-784-990-10	Sequence 10, Appl
15	1362.8	40.6	1662	15	US-10-229-412-10	Sequence 10, Appl
16	1160.8	34.6	1716	9	US-09-784-990-7	Sequence 7, Appli
17	1160.8	34.6	1716	15	US-10-229-412-7	Sequence 7, Appli
18	831.2	24.8	1753	20	US-10-839-509-1	Sequence 1, Appli
19	819.2	24.4	1753	21	US-10-838-834-12	Sequence 12, Appl
20	819.2	24.4	10603	21	US-10-838-834-26	Sequence 26, Appl
c	819.2	24.4	10603	21	US-10-838-834-25	Sequence 25, Appl
c	819.2	24.4	10677	21	US-10-838-834-1	Sequence 1, Appli
22	816.2	24.3	1760	21	US-10-838-834-1	Sequence 1, Appli
23	149.6	4.5	15498	9	US-09-733-692A-61	Sequence 61, Appl
24	148	4.4	15654	20	US-10-667-141-60	Sequence 60, Appl
25	147.6	4.4	15654	20	US-10-667-141-59	Sequence 59, Appl
26	145.8	4.3	15492	9	US-09-733-692A-60	Sequence 60, Appl
27	145.8	4.3	15492	9	US-09-733-692A-62	Sequence 62, Appl
28	142.6	4.2	15654	20	US-10-667-141-58	Sequence 58, Appl
29	139.4	4.2	1500	16	US-10-377-718-9	Sequence 9, Appli
30	139.4	4.2	1500	17	US-10-429-735-9	Sequence 9, Appli
31	96.8	2.9	1617	22	US-10-842-032-25	Sequence 25, Appl
32	96.8	2.9	1844	22	US-10-842-032-1	Sequence 1, Appli
33	96	2.9	1986	18	US-10-670-695-35	Sequence 35, Appl
34	96	2.9	2113	10	US-09-951-061A-86	Sequence 86, Appl
c	96	2.9	4343	10	US-09-951-061A-91	Sequence 91, Appl
c	96	2.9	4604	10	US-09-951-061A-93	Sequence 93, Appl
37	96	2.9	15690	21	US-10-312-052B-1	Sequence 1, Appli
38	96	2.9	15690	21	US-10-312-052B-2	Sequence 2, Appli
39	96	2.9	18826	21	US-10-312-052B-3	Sequence 3, Appli
40	87.8	2.6	692	15	US-10-206-901B-50	Sequence 50, Appl
41	83.4	2.5	2384	17	US-10-397-635-8	Sequence 8, Appli
42	82	2.4	1653	9	US-09-873-233A-17	Sequence 17, Appl
43	79.4	2.4	1653	9	US-09-873-233A-19	Sequence 19, Appl
44	79.2	2.4	15456	10	US-09-900-112-35	Sequence 35, Appl
45	79.2	2.4	15456	10	US-09-900-112-36	Sequence 36, Appl

ALIGNMENTS

RESULT 1
US-10-800-256-1
; Sequence 1, Application US/10800256
; Publication No. US20050031642A1
; GENERAL INFORMATION:
; APPLICANT: Zakay-Kones, Zichria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF CANCER
; FILE REFERENCE: 85189-5900
; CURRENT APPLICATION NUMBER: US/10/800,256
; CURRENT FILING DATE: 2004-03-11
; PRIOR APPLICATION NUMBER: IL 145397
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: IL 145397
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 3358
; TYPE: DNA
; ORGANISM: Newcastle disease virus
US-10-800-256-1

Query Match 100.0%; Score 3358; DB 21; Length 3358;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3358; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	601	TGTTAATGACCAATTTAATAAACAAGCTCAGGAATTAGACTGCATCAAAATTCACAGCA	660
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QY	661	AGTTGGTGTAGAGCTCAACTGACCTTAACCGAATTGACTACAGTATTCGGAACCAAAAT	720
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QY	841	TAGCGGCTTAATCACCGGTAACCTTATCTATACGACTCACAGACTCAACTCTTGGGTAT	900
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Db 2761 GAAAGGACCTAGATGTCACAACTTATTCGGGACTGGGTGCGCAACTACCCAGGAGTA 2820
Qy 2821 GGGGTTGGATCTTTTATTGACAGCGCGGTATGTTCTCAGTCTACGGAGGTTAAACCC 2880
Db 2821 GGGGTTGGATCTTTTATTGACAGCGCGGTATGTTCTCAGTCTACGGAGGTTAAACCC 2880
Qy 2881 AATTCAACCGATGACACTGACAGGAAGGGAATATGTGATATACAGCGATACATGAC 2940
Db 2881 AATTCAACCGATGACACTGACAGGAAGGGAATATGTGATATACAGCGATACATGAC 2940
Qy 2941 ACATGCCAGATGACAGACTACAGATTCGATGCGCAAGTCTTCGTATAGCCCTGGA 3000
Db 2941 ACATGCCAGATGACAGACTACAGATTCGATGCGCAAGTCTTCGTATAGCCCTGGA 3000
Qy 3001 CGGTTTGGTGGAAACGATACAGCAGGCTATCTTATCTATCAAGGTGTCAACATCCTTA 3060
Db 3001 CGGTTTGGTGGAAACGATACAGCAGGCTATCTTATCTATCAAGGTGTCAACATCCTTA 3060
Qy 3061 GGGGAAGACCGGTACTGATGTAACGCCCAACACAGTCACTCATGCGGGGCGGAAGGC 3120
Db 3061 GGGGAAGACCGGTACTGATGTAACGCCCAACACAGTCACTCATGCGGGGCGGAAGGC 3120
Qy 3121 AGAATTCACAGTAGGACATCTCATTTCTTGTATCAACGAGGTCATCATCTTCT 3180
Db 3121 AGAATTCACAGTAGGACATCTCATTTCTTGTATCAACGAGGTCATCATCTTCT 3180
Qy 3181 CCGCGTTATTATATCTATGACAGTACAGCAAAACAGGCACTCTTTCATAGTCTTAT 3240
Db 3181 CCGCGTTATTATATCTATGACAGTACAGCAAAACAGGCACTCTTTCATAGTCTTAT 3240
Qy 3241 ACATTCAATGCTTCACTCGGCCAGGTAGTATCCCTTCCAGGCTTCAGCAAGATGCCCC 3300
Db 3241 ACATTCAATGCTTCACTCGGCCAGGTAGTATCCCTTCCAGGCTTCAGCAAGATGCCCC 3300
Qy 3301 AACTCGTGTGTACTGAGTCTATACAGATCCATATCCCTTAATCTTCTATAGAAACC 3358
Db 3301 AACTCGTGTGTACTGAGTCTATACAGATCCATATCCCTTAATCTTCTATAGAAACC 3358

RESULT 2

US-09-741-744A-134
; Sequence 134, Application US/09741744A
; Publication No. US20030087417A1
; GENERAL INFORMATION:
; APPLICANT: Peeters, Bernadus
; APPLICANT: de Leeuw, Olav
; APPLICANT: Klaus, Guss
; APPLICANT: Arnoud, Gielkens
; TITLE OF INVENTION: Newcastle Disease Virus Infectious Clones, Vaccines and Diagnosti
; FILE REFERENCE: 2183-4646US
; CURRENT APPLICATION NUMBER: US/09/741,744A
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: PCT/NL99/00377
; PRIOR FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 134
; TYPE: DNA
; LENGTH: 15186
; ORGANISM: Newcastle disease virus LaSota
US-09-741-744A-134

Query Match 99.9%; Score 3353.2; DB 10; Length 15186;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3355; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ACGGTTAGAGATTCTGGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACC 60
Db 4498 ACGGTTAGAGATTCTGGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACC 4557
Qy 61 TTCTACCAAGAACCCAGCACCTATGATGCTGACTATCCGGGTTGCGCTGGCACTGAGTTG 120
Db 4558 TTCTACCAAGAACCCAGCACCTATGATGCTGACTATCCGGGTTGCGCTGGCACTGAGTTG 4617
Qy 121 CATCTGTCCGGCAAACTCCATTGATGGCAGCCCTTTGAGCTGCAGAAATTGGTTTAC 180
Db 4618 CATCTGTCCGGCAAACTCCATTGATGGCAGCCCTTTGAGCTGCAGAAATTGGTTTAC 4677
Qy 181 AGAGCAAAAGCCGTCAACATATACACCTCATCCAGACAGGATCAATCATAGTTAAGCT 240
Db 4678 AGAGCAAAAGCCGTCAACATATACACCTCATCCAGACAGGATCAATCATAGTTAAGCT 4737
Qy 241 CCTCCCGAATCTGCCAAGGATAAGAGGATGTGCGAAAGCCCTTTGGATGCATACAA 300
Db 4738 CCTCCCGAATCTGCCAAGGATAAGAGGATGTGCGAAAGCCCTTTGGATGCATACAA 4797
Qy 301 CAGGACATTGACCACTTTGTCTACCCCTTTGGTGACTCTATCGGTAGGATACAAGAGTC 360
Db 4798 CAGGACATTGACCACTTTGTCTACCCCTTTGGTGACTCTATCGGTAGGATACAAGAGTC 4857
Qy 361 TGTGACTACATCTGGAGGGGGAGACAGGGCGGCTTATAGGCGCCATTTGGCGGCTGT 420
Db 4858 TGTGACTACATCTGGAGGGGGAGACAGGGCGGCTTATAGGCGCCATTTGGCGGCTGT 4917
Qy 421 GGCTCTTGGGTTGCAACTGCCGCACAAATAACAGCGCGCCGAGCTCTGATACAAAGCAA 480
Db 4918 GGCTCTTGGGTTGCAACTGCCGCACAAATAACAGCGCGCCGAGCTCTGATACAAAGCAA 4977
Qy 481 ACAAATGTGCCAACAATCTCCGACTTAAAGAGAGCAATTTGCCGCAACCAATAGGCTGT 540
Db 4978 ACAAATGTGCCAACAATCTCCGACTTAAAGAGAGCAATTTGCCGCAACCAATAGGCTGT 5037
Qy 541 GCATGAGGTCACTGACGGATTATCGCAACTAGCAGTGGCAGTTGGGAGATGCGAGCAGTT 600
Db 5038 GCATGAGGTCACTGACGGATTATCGCAACTAGCAGTGGCAGTTGGGAGATGCGAGCAGTT 5097
Qy 601 TGTTAATGACCAATTTTAATAAACAAGCTCAGGAAATTAGACTGCAATCAAAATTGACAGCA 660
Db 5098 TGTTAATGACCAATTTTAATAAACAAGCTCAGGAAATTAGACTGCAATCAAAATTGACAGCA 5157

QY	661	AGTTGGTGTAGAGCTCAACCTGTACTTAACCGAATTGACTACAGTATTGCGACCACAAAAT	720
Db	5158	AGTTGGTGTAGAGCTCAACCTGTACTTAACCGAATTGACTACAGTATTGCGACCACAAAAT	5217
QY	721	CACCTTACCCTGCTTTAAACAGCTGACTATTACGGCACTTTTCAATCTAGCTGCTGGAAA	780
Db	5218	CACCTTACCCTGCTTTAAACAGCTGACTATTACGGCACTTTTCAATCTAGCTGCTGGAAA	5277
QY	781	TATGGATTACTTATTTGACTAAGTTAGGTGTAGGGAACAATCAACTCAGCTCATTAATCGG	840
Db	5278	TATGGATTACTTATTTGACTAAGTTAGGTGTAGGGAACAATCAACTCAGCTCATTAATCGG	5337
QY	841	TAGCGGCTTAATCACCGGTAAACCTTATTTATACGACTCACAGACTCAACTCTTGGGTAT	900
Db	5338	TAGCGGCTTAATCACCGGTAAACCTTATTTATACGACTCACAGACTCAACTCTTGGGTAT	5397
QY	901	ACAGGTTAACTCTACCTTCACTCGGGAACCTTAATAATATATGCGTGCACCTACTTGAAC	960
Db	5398	ACAGGTTAACTCTACCTTCACTCGGGAACCTTAATAATATATGCGTGCACCTACTTGAAC	5457
QY	961	CTTATCCGTAAGCACCAACAGGGGATTTGCTCGGCACCTTGTCCTCAAAAGTGGTGACACA	1020
Db	5458	CTTATCCGTAAGCACCAACAGGGGATTTGCTCGGCACCTTGTCCTCAAAAGTGGTGACACA	5517
QY	1021	GGTCCGTTCTGTGATAGAACTTGACACCTCATCTGTATAGAACTGACTTAGATT	1080
Db	5518	GGTCCGTTCTGTGATAGAACTTGACACCTCATCTGTATAGAACTGACTTAGATT	5577
QY	1081	ATATTGTACAAGTAAGTAACGTTTCCCTATGTCCTCGGTATTTATTTCTGCTTGAGCGG	1140
Db	5578	ATATTGTACAAGTAAGTAACGTTTCCCTATGTCCTCGGTATTTATTTCTGCTTGAGCGG	5637
QY	1141	CAATAGCTCGGCTGTATGACTCAAGACCGAAGCGCACTTACTACACCATACATGAC	1200
Db	5638	CAATAGCTCGGCTGTATGACTCAAGACCGAAGCGCACTTACTACACCATACATGAC	5697
QY	1201	TATCAAGGTTTCAGTTCATCGCCAACTGCAAGATGACAACTGTAGATGTGTAAACCCCCC	1260
Db	5698	TATCAAGGTTTCAGTTCATCGCCAACTGCAAGATGACAACTGTAGATGTGTAAACCCCCC	5757
QY	1261	GGGTATCATATCGCAAACTATGAGAGAGCGGTGCTCTAATAGATAAACAATCATGCAA	1320
Db	5758	GGGTATCATATCGCAAACTATGAGAGAGCGGTGCTCTAATAGATAAACAATCATGCAA	5817
QY	1321	TGTTTTATCTTAGGGGGGATACTTTTAAGGCTCAGTGGGGAAATTCGATCTAATCTATCA	1380
Db	5818	TGTTTTATCTTAGGGGGGATACTTTAAGGCTCAGTGGGGAAATTCGATCTAATCTATCA	5877
QY	1381	GAAGAATATCTCAATACAAGATTCTCAAGTAATAATAACAGGCAATCTTGATATCTCAAC	1440
Db	5878	GAAGAATATCTCAATACAAGATTCTCAAGTAATAATAACAGGCAATCTTGATATCTCAAC	5937
QY	1441	TGAGCTTGGGAATGTCAAACCTCGATCAGTAATGCTTTGAAATAAGTTAGAGAAAGCAA	1500
Db	5938	TGAGCTTGGGAATGTCAAACCTCGATCAGTAATGCTTTGAAATAAGTTAGAGAAAGCAA	5997
QY	1501	CAGAAACTAGACAAAGTCAATGTCAAACCTGACACATCTGCTCATTAATCACTATAT	1560
Db	5998	CAGAAACTAGACAAAGTCAATGTCAAACCTGACACATCTGCTCATTAATCACTATAT	6057
QY	1561	CGTTTTGACTATCATATCTCTTTTGGTATACCTTAGCCCTGATTTCTAGCATGCTACCT	1620
Db	6058	CGTTTTGACTATCATATCTCTTTTGGTATACCTTAGCCCTGATTTCTAGCATGCTACCT	6117
QY	1621	AATGTACAAGCAAAAGCGCAACAAAACCTTATTTATGCTTGGGAATAATATCTCTAGA	1680
Db	6118	AATGTACAAGCAAAAGCGCAACAAAACCTTATTTATGCTTGGGAATAATATCTCTAGA	6177
QY	1681	TCAGATGAGAGCCACTACAAAATGTGAACACAGATGAGGAACGAAGTTTCCCTAATAG	1740
Db	6178	TCAGATGAGAGCCACTACAAAATGTGAACACAGATGAGGAACGAAGTTTCCCTAATAG	6237
QY	1741	TAATTTTGTGTGAAGTTCTCGGTAGTCTGTCAAGTTTACAGAGAGTTAAGAAAAAACTACCGGT	1800

Db	6238	TAATTTGTGTGAAGTTCTCGGTAGTCTGTCAAGTTTACAGAGAGTTAAGAAAAAACTACCGGT	6297
QY	1801	TGTAGATGACCAAAAGGACGATATACGGGTAGAACGGTAAGAGAGGCGCCCTCAATTGC	1860
Db	6298	TGTAGATGACCAAAAGGACGATATACGGGTAGAACGGTAAGAGAGGCGCCCTCAATTGC	6357
QY	1861	GAGCCAGGCTTCAACAACCTCCGTTCTACCGCTTCCACGCAACAGTCTCAATCATGGAC	1920
Db	6358	GAGCCAGGCTTCAACAACCTCCGTTCTACCGCTTCCACGCAACAGTCTCAATCATGGAC	6417
QY	1921	CGCGCGTTAGCCAAAGTTGCGTTAGAGAATGATGAAAGAGAGGCAAAAAATATACGCGCG	1980
Db	6418	CGCGCGTTAGCCAAAGTTGCGTTAGAGAATGATGAAAGAGAGGCAAAAAATATACGCGCG	6477
QY	1981	TTGATATTCGCGATTGCAATCTTATTTAAACAGTAGTGACCTTGCTGTATCTGTAGCC	2040
Db	6478	TTGATATTCGCGATTGCAATCTTATTTAAACAGTAGTGACCTTGCTGTATCTGTAGCC	6537
QY	2041	TCCTTTTATATAGCATGGGGCTAGCACACCTAGCGATCTTTGTAGGCATACCGACTAGG	2100
Db	6538	TCCTTTTATATAGCATGGGGCTAGCACACCTAGCGATCTTTGTAGGCATACCGACTAGG	6597
QY	2101	ATTTCCAGGCGAGAGAAAAGATTACATCTACACTTTGGTTCCATCAAGATGTAGTAGAT	2160
Db	6598	ATTTCCAGGCGAGAGAAAAGATTACATCTACACTTTGGTTCCATCAAGATGTAGTAGAT	6657
QY	2161	AGGATATATAACAGTAGTGCGCTTGGTCTCGTTGGCATTTGTAATAACTGAGACACA	2220
Db	6658	AGGATATATAACAGTAGTGCGCTTGGTCTCGTTGGCATTTGTAATAACTGAGACACA	6717
QY	2221	ATTATGAACGCAATAACATCTCTCTTATCAGATTAATGGAGCTGCAAAACAGTGGG	2280
Db	6718	ATTATGAACGCAATAACATCTCTCTTATCAGATTAATGGAGCTGCAAAACAGTGGG	6777
QY	2281	TGGGGGCGACTTATCCATGCCAGATTATATAGGGGGGATAGGCAAGAACTCATTTGTA	2340
Db	6778	TGGGGGCGACTTATCCATGCCAGATTATATAGGGGGGATAGGCAAGAACTCATTTGTA	6837
QY	2341	GATGATGCTAGTGTGATGTCATCATCTATCCCTCTGCAATTTCAAGAAACATCTGAATTTT	2400
Db	6838	GATGATGCTAGTGTGATGTCATCATCTATCCCTCTGCAATTTCAAGAAACATCTGAATTTT	6897
QY	2401	ATCCCGCGCTACTACAGGATCAGGTTGCACTCGAATACCCCTCATTTGACATGAGTGCT	2460
Db	6898	ATCCCGCGCTACTACAGGATCAGGTTGCACTCGAATACCCCTCATTTGACATGAGTGCT	6957
QY	2461	ACCATACTGCTACACCCATTAATGTAATATTTGCTGGAATGACAGATCACTCACAATCA	2520
Db	6958	ACCATACTGCTACACCCATTAATGTAATATTTGCTGGAATGACAGATCACTCACAATCA	7017
QY	2521	TATCAGTATTTAGCACTTGTGCTCCGACATCTGCAACAGGAGGGTATTTCTTTTCT	2580
Db	7018	TATCAGTATTTAGCACTTGTGCTCCGACATCTGCAACAGGAGGGTATTTCTTTTCT	7077
QY	2581	ACTCTCCGTTTCCATCAACCTGACACACCCAAAATCGGAAGTCTTTCAGTGTGAGTGA	2640
Db	7078	ACTCTCCGTTTCCATCAACCTGACACACCCAAAATCGGAAGTCTTTCAGTGTGAGTGA	7137
QY	2641	ACTCCCTCGGTTGTGATATGCTGCTCGAAAGTCAACGAGACACAGGAGAAAGATTAT	2700
Db	7138	ACTCCCTCGGTTGTGATATGCTGCTCGAAAGTCAACGAGACACAGGAGAAAGATTAT	7197
QY	2701	AACCTCAGTGTCCCTACGCGGATGTTACATGGGAGGTAGGGTTCCACGCGCAGTACCAC	2760
Db	7198	AACCTCAGTGTCCCTACGCGGATGTTACATGGGAGGTAGGGTTCCACGCGCAGTACCAC	7257
QY	2761	GAAAAGGACCTAGATGTCACAACTTATTTCCGGGGAATGCGGTGGCCCAACTACCCAGGATA	2820
Db	7258	GAAAAGGACCTAGATGTCACAACTTATTTCCGGGGAATGCGGTGGCCCAACTACCCAGGATA	7317
QY	2821	GGGGGTGGAATCTTTTATTTGACAGCCCGGTATGGTTCTCAGTCTACGAGGGTTAAACCC	2880

Db 7318 GGGGGTGGATCTTTTATTGACAGCGCGTATGTTTCTCAGTCTACGGAGGGTTAAACCC 7377
Qy 2881 AATTACCCAGTGACACTGTACAGAAAGGAAATATGTATATACAGCCGATCAATGAC 2940
Db 7378 AATTACCCAGTGACACTGTACAGAAAGGAAATATGTATATACAGCCGATCAATGAC 7437
Qy 2941 ACATGCCCAGATGACAAAGACTTACAGATTCGAATGGCCAAAGTCTTCGTATAAGCCTGGA 3000
Db 7438 ACATGCCCAGATGACAAAGACTTACAGATTCGAATGGCCAAAGTCTTCGTATAAGCCTGGA 7497
Qy 3001 CGGTTTGGTGGAAACGCATACAGCAGGCTATCTTATCTATCAAGGTTGTCAACATCTTTA 3060
Db 7498 CGGTTTGGTGGAAACGCATACAGCAGGCTATCTTATCTATCAAGGTTGTCAACATCTTTA 7557
Qy 3061 GCGGAAGACCGGTACTGACTGTACCGCCCAACACAGTCACTCATGGGGCCGAAGGC 3120
Db 7558 GCGGAAGACCGGTACTGACTGTACCGCCCAACACAGTCACTCATGGGGCCGAAGGC 7617
Qy 3121 AGAATCTCACAGTAGGACATCTCATTTCTTGTATCAACGAGGTCATCATCTTCT 3180
Db 7618 AGAATCTCACAGTAGGACATCTCATTTCTTGTATCAACGAGGTCATCATCTTCT 7677
Qy 3181 CCCGGTTATTATATCTTATGACAGTCAAGCAACAAACAGCCACTCTTTCATAGTCTTTAT 3240
Db 7678 CCCGGTTATTATATCTTATGACAGTCAAGCAACAAACAGCCACTCTTTCATAGTCTTTAT 7737
Qy 3241 ACATTCATAGCTTCACTCGGCCAGGTAGTATCCCTTCCAGGCTTCAGCAAGTATGCC 3300
Db 7738 ACATTCATAGCTTCACTCGGCCAGGTAGTATCCCTTCCAGGCTTCAGCAAGTATGCC 7797
Qy 3301 AACTCGTGTACTGGAGTCTATACAGATCCATATCCCTTAATCTTATAGAAACC 3358
Db 7798 AACTCGTGTACTGGAGTCTATACAGATCCATATCCCTTAATCTTATAGAAACC 7855

RESULT 3

US-10-377-718-3

; Sequence 3, Application US/10377718

; Publication No. US20030175291A1

; GENERAL INFORMATION:

; APPLICANT: KUO, Tsun Yuang

; TITLE OF INVENTION: MULTIPLE AND MULTIVALENT DNA VACCINES IN OVO

; FILE REFERENCE: 39734-186920

; CURRENT APPLICATION NUMBER: US/10/377,718

; CURRENT FILING DATE: 2003-03-04

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 3

; LENGTH: 15186

; TYPE: DNA

; ORGANISM: Newcastle disease virus (NDV)

US-10-377-718-3

Query Match 99.9%; Score 3353.2; DB 16; Length 15186;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 3355; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ACGGGTAGAAGATTCTGGATCCGGTGGCCCTCCAGGTGCAAGATGGGCTCCAGACC 60
Db 4498 ACGGGTAGAAGATTCTGGATCCGGTGGCCCTCCAGGTGCAAGATGGGCTCCAGACC 4557
Qy 61 TTCTACCAAGAACCCAGCACTATGATGCTGACTATCCGGGTTCGGCTGGCACTGAGTTG 120
Db 4558 TTCTACCAAGAACCCAGCACTATGATGCTGACTATCCGGGTTCGGCTGGCTGACTGAGTTG 4617
Qy 121 CATCTGCCGCAAACTCCATTGATGGCAGGCTCTTCAGCTGCAGGAATTTGGTTAC 180
Db 4618 CATCTGCCGCAAACTCCATTGATGGCAGGCTCTTCAGCTGCAGGAATTTGGTTAC 4677
Qy 181 AGGAGACAAAGCCGTCAACATATACCTATCCAGACAGGATCAATAGTTAAGCT 240
Db 4678 AGGAGACAAAGCCGTCAACATATACCTATCCAGACAGGATCAATAGTTAAGCT 4737

Qy 241 CCTCCGAATCTGCCAAGGATAGGAGGCATGTGCGAAAGCCCCCTTGGATGCATACAA 300
Db 4738 CCTCCGAATCTGCCAAGGATAGGAGGCATGTGCGAAAGCCCCCTTGGATGCATACAA 4797
Qy 301 CAGGACATTTGACCACTTTTGTCTCACCCCCCTTTGGTGACTCTATCCGTAGGATACAGAGTC 360
Db 4798 CAGGACATTTGACCACTTTTGTCTCACCCCCCTTTGGTGACTCTATCCGTAGGATACAGAGTC 4857
Qy 361 TGTGACTACATCTGGAGGGGGAGACAGGGGGCGCTTATAGGCGCCATTTATGGCGGTGT 420
Db 4858 TGTGACTACATCTGGAGGGGGAGACAGGGGGCGCTTATAGGCGCCATTTATGGCGGTGT 4917
Qy 421 GGCTCTTGGGGTTCGAACCTCCGCAAAATAAAGAGAGCAATTTGCCGCAACCAATAGGCGTGT 540
Db 4918 GGCTCTTGGGGTTCGAACCTCCGCAAAATAAAGAGAGCAATTTGCCGCAACCAATAGGCGTGT 4977
Qy 481 ACAAATAGCTGCCAAACATCTCCGACTTAAAGAGAGCAATTTGCCGCAACCAATAGGCGTGT 540
Db 4978 ACAAATAGCTGCCAAACATCTCCGACTTAAAGAGAGCAATTTGCCGCAACCAATAGGCGTGT 5037
Qy 541 GCATGAGTCACTGACCGGATTTATCGCAACTAGCAGTGGCAGTTGGGAAGATGCGAGCTGT 600
Db 5038 GCATGAGTCACTGACCGGATTTATCGCAACTAGCAGTGGCAGTTGGGAAGATGCGAGCTGT 5097
Qy 601 TGTTAATGACCAATTTTAAACAGCTTCAGGATTTAGACTGCAATCAAAATGCGACAGCA 660
Db 5098 TGTTAATGACCAATTTTAAACAGCTTCAGGATTTAGACTGCAATCAAAATGCGACAGCA 5157
Qy 661 AGTTGGTGTAGAGTCAACCTGTACCTAAACGAATTCAGTACAGTATTCGAGCCACCAAT 720
Db 5158 AGTTGGTGTAGAGTCAACCTGTACCTAAACGAATTCAGTATTCGAGCCACCAAT 5217
Qy 721 CACTTCACCTGCTTAAACAGCTGACTATTTACGGCACTTTTCAATCTAGCTGGTGAAA 780
Db 5218 CACTTCACCTGCTTAAACAGCTGACTATTTACGGCACTTTTCAATCTAGCTGGTGAAA 5277
Qy 781 TATGGATTACTTATTTAGTAAAGTTAGTGTAGGGAACAATCACTCAGCTCATTAATCGG 840
Db 5278 TATGGATTACTTATTTAGTAAAGTTAGTGTAGGGAACAATCACTCAGCTCATTAATCGG 5337
Qy 841 TAGCGGCTTAATCACCGGTAAACCTTCTATACGACTCACAGACTCAACTCTTTGGGTAT 900
Db 5338 TAGCGGCTTAATCACCGGTAAACCTTCTATACGACTCACAGACTCAACTCTTTGGGTAT 5397
Qy 901 ACAGGTAACCTCTACCTTCAGTTCGGGAACCTTAAATAATATGCGTGCCCACTTCTGGAAC 960
Db 5398 ACAGGTAACCTCTACCTTCAGTTCGGGAACCTTAAATAATATGCGTGCCCACTTCTGGAAC 5457
Qy 961 CTTATCCGTAAAGCAACACAGGGGATTTGGCTCGGCACTTTGTCCCAAAAGTGTGACACA 1020
Db 5458 CTTATCCGTAAAGCAACACAGGGGATTTGGCTCGGCACTTTGTCCCAAAAGTGTGACACA 5517
Qy 1021 GGTCGGTTCGTGATAGAAACCTTGACACTCATCTGATATAGAACTGACTTAGATTT 1080
Db 5518 GGTCGGTTCGTGATAGAAACCTTGACACTCATCTGATATAGAACTGACTTAGATTT 5577
Qy 1081 ATATTGTACAAAGATAGTAAACCTTCCCTATGTCCCTGGTATTTATTCCTGCTTGAGCGG 1140
Db 5578 ATATTGTACAAAGATAGTAAACCTTCCCTATGTCCCTGGTATTTATTCCTGCTTGAGCGG 5637
Qy 1141 CAATACTCGGCTGTATGATCTCAAAAGACCGAAGGCGCACTTACTACACATACATGAC 1200
Db 5638 CAATACTCGGCTGTATGATCTCAAAAGACCGAAGGCGCACTTACTACACATACATGAC 5697
Qy 1201 TATCAAGGTTCACTGATCGCCAACTGCAAGATGACAACTAGATGTGTAAACCCCC 1260
Db 5698 TATCAAGGTTCACTGATCGCCAACTGCAAGATGACAACTAGATGTGTAAACCCCC 5757
Qy 1261 GGGTATCATATCGCAAACTATCGAGAAAGCGGTGTCTCTAATAGATAAAACATCATGCAA 1320
Db 5758 GGGTATCATATCGCAAACTATCGAGAAAGCGGTGTCTCTAATAGATAAAACATCATGCAA 5817
Qy 1321 TGTTTTATCCTTAGGGGGATAAATTTTAAAGGCTCAGTGGGGAAATTCGATGTAACTTATCA 1380

; CURRENT FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 15186
; TYPE: DNA
; ORGANISM: Newcastle disease virus (NDV)
US-10-429-735-3

Query Match 99.9%; Score 3353.2; DB 17; Length 15186;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3355; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	1	ACGGGTAGAGATTCTGGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACC	60
Db	4498	ACGGGTAGAGATTCTGGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACC	4557
Qy	61	TTCTACCAAGAACCCAGCACCTATGATGCTGACTATCCGGTTCGGCTGGGCACCTGAGTTG	120
Db	4558	TTCTACCAAGAACCCAGCACCTATGATGCTGACTATCCGGTTCGGCTGGGCACCTGAGTTG	4617
Qy	121	CATCTGTCGGCAAACTCCATTGATGGCAGGCTCTTTCGAGCTGCAGGAAATTTGGTTAC	180
Db	4618	CATCTGTCGGCAAACTCCATTGATGGCAGGCTCTTTCGAGCTGCAGGAAATTTGGTTAC	4677
Qy	181	AGGAGACAAAGCCCTCAACATATACCTCATCCAGACAGGATCAATCATAGTTAAGCT	240
Db	4678	AGGAGACAAAGCCCTCAACATATACCTCATCCAGACAGGATCAATCATAGTTAAGCT	4737
Qy	241	CCTCCGAAATCTGCCAAGGATAGGAGGCAATGTCGAAAGCCCTTGGATGCATACAA	300
Db	4738	CCTCCGAAATCTGCCAAGGATAGGAGGCAATGTCGAAAGCCCTTGGATGCATACAA	4797
Qy	301	CAGACATTGACCACTTTGCTCACCCCTTGGTGACTCTATCCGTAGGATACAAAGATC	360
Db	4798	CAGACATTGACCACTTTGCTCACCCCTTGGTGACTCTATCCGTAGGATACAAAGATC	4857
Qy	361	TGTCATCATCTCGAGGGGGGAGACAGGGGCGCTTATAGGCGCCATTAATGGCGGTGT	420
Db	4858	TGTCATCATCTCGAGGGGGGAGACAGGGGCGCTTATAGGCGCCATTAATGGCGGTGT	4917
Qy	421	GGCTCTTGGGTTGCAACTGCGGCACAAATAACAGCGCGCCAGCTCTGTACAGCCAA	480
Db	4918	GGCTCTTGGGTTGCAACTGCGGCACAAATAACAGCGCGCCAGCTCTGTACAGCCAA	4977
Qy	481	ACAAATGCTGCCAACAATCTCCGACTTAAAGAGAGCAATTCGCCAACAATGAGGCTGT	540
Db	4978	ACAAATGCTGCCAACAATCTCCGACTTAAAGAGAGCAATTCGCCAACAATGAGGCTGT	5037
Qy	541	GCATGAGGTCACTGACGGATTATCGCAACTAGCAGTGGCAGTTGGGAAGATGCAAGCTT	600
Db	5038	GCATGAGGTCACTGACGGATTATCGCAACTAGCAGTGGCAGTTGGGAAGATGCAAGCTT	5097
Qy	601	TGTTAATGACCAATTTAATAAACAAGCTCAGGAATTAGATGCAATTAATGCAAGCA	660
Db	5098	TGTTAATGACCAATTTAATAAACAAGCTCAGGAATTAGATGCAATTAATGCAAGCA	5157
Qy	661	AGTTGGTGTAGAGCTCAACCTGACCTAACCGAATTCAGCTACAGTATTTCGGACCAAAAT	720
Db	5158	AGTTGGTGTAGAGCTCAACCTGACCTAACCGAATTCAGCTACAGTATTTCGGACCAAAAT	5217
Qy	721	CACCTTCACCTCTTTAAACAAGCTGACTATTTCAGGCACTTTTACAATCTAGCTGGTGA	780
Db	5218	CACCTTCACCTCTTTAAACAAGCTGACTATTTCAGGCACTTTTACAATCTAGCTGGTGA	5277
Qy	781	TATGGAATTAATGATTAAGTATAGGTAGGTAGGGAACAACTCACTGACTCAATTAATCGG	840
Db	5278	TATGGAATTAATGATTAAGTATAGGTAGGTAGGGAACAACTCACTGACTCAATTAATCGG	5337
Qy	841	TAGCGGCTTAATCACCGGTAAACCTTCTATACGCTCACAGACTCAACTCTTGGGTAT	900
Db	5338	TAGCGGCTTAATCACCGGTAAACCTTCTATACGCTCACAGACTCAACTCTTGGGTAT	5397

Qy	901	ACAGGTAACCTCAGTTCGGTACCTAAATATATATCGTGCCACCTACTTGGAAAC	960
Db	5398	ACAGGTAACCTCAGTTCGGTACCTAAATATATATCGTGCCACCTACTTGGAAAC	5457
Qy	961	CTTATCCGTAAGCAACACAGGGGATTGGCTCGGCACCTTGTCCCAAAGTGGTGACACA	1020
Db	5458	CTTATCCGTAAGCAACACAGGGGATTGGCTCGGCACCTTGTCCCAAAGTGGTGACACA	5517
Qy	1021	GGTCGGTTCGTGATAGAGAACTTGACACCTCATCTGATATAGAAAATGACTGTAGATTT	1080
Db	5518	GGTCGGTTCGTGATAGAGAACTTGACACCTCATCTGATATAGAAAATGACTGTAGATTT	5577
Qy	1081	ATATTGTACAGAAATAGTAACGTTCCCTATGTCCCTGGTATTTATTCCTGCTTGAGCGG	1140
Db	5578	ATATTGTACAGAAATAGTAACGTTCCCTATGTCCCTGGTATTTATTCCTGCTTGAGCGG	5637
Qy	1141	CAATACGTCGGCTGTATGTACTCAAGACCGAAGCGCACTTACTACACCATACATGAC	1200
Db	5638	CAATACGTCGGCTGTATGTACTCAAGACCGAAGCGCACTTACTACACCATACATGAC	5697
Qy	1201	TATCAAAAGGTTCAAGTCATCCGCAACTGCAAGATGACAAATGTAGATGTGTAAACCCGCC	1260
Db	5698	TATCAAAAGGTTCAAGTCATCCGCAACTGCAAGATGACAAATGTAGATGTGTAAACCCGCC	5757
Qy	1261	GGGTATCATATCGCAAACTATGGAGAGCGGTGTCTTAATAGATAAAACAATCATGCAA	1320
Db	5758	GGGTATCATATCGCAAACTATGGAGAGCGGTGTCTTAATAGATAAAACAATCATGCAA	5817
Qy	1321	TGTTTATCTTGAAGGGGATACTTAAAGCTCAGTGGGGAATTCGATGTAACTTATCA	1380
Db	5818	TGTTTATCTTGAAGGGGATACTTAAAGCTCAGTGGGGAATTCGATGTAACTTATCA	5877
Qy	1381	GAAGAAATATCTCAATCAAGATTCTCAAGTAATAATAACAGGCAATCTTGATATCTCAAC	1440
Db	5878	GAAGAAATATCTCAATCAAGATTCTCAAGTAATAATAACAGGCAATCTTGATATCTCAAC	5937
Qy	1441	TGAGCTTGGGAATGTCAAACTCGATCAGTAATGCTTGAATAAGTTAGAGGAAGCAA	1500
Db	5938	TGAGCTTGGGAATGTCAAACTCGATCAGTAATGCTTGAATAAGTTAGAGGAAGCAA	5997
Qy	1501	CAGAAAATAGACAAAGTCAATGTCAAACTGACTAGCACATCTGCTCTCTATCTATAT	1560
Db	5998	CAGAAAATAGACAAAGTCAATGTCAAACTGACTAGCACATCTGCTCTCTATCTATAT	6057
Qy	1561	CGTTTGAATCATATCTCTTGTGTTTGGTATATCTTAGCCTGATTTAGCATGCTACCT	1620
Db	6058	CGTTTGAATCATATCTCTTGTGTTTGGTATATCTTAGCCTGATTTAGCATGCTACCT	6117
Qy	1621	ATGTACAGCAAAAGCGCAACAAAAAACCTTATATGCTTGGGAATTAATCTCTAGA	1680
Db	6118	ATGTACAGCAAAAGCGCAACAAAAAACCTTATATGCTTGGGAATTAATCTCTAGA	6177
Qy	1681	TCAGATGAGAGCCACTACAAAAATGTGAAACACAGATGAGGAACGAAGTTTCCCTAATAG	1740
Db	6178	TCAGATGAGAGCCACTACAAAAATGTGAAACACAGATGAGGAACGAAGTTTCCCTAATAG	6237
Qy	1741	TAATTTGTGTGAAAGTTCTGCTAGTCTGTGAGTTTCAAGAGTTTAAAGAAAAAATACCGGT	1800
Db	6238	TAATTTGTGTGAAAGTTCTGCTAGTCTGTGAGTTTCAAGAGTTTAAAGAAAAAATACCGGT	6297
Qy	1801	TGTAGATGACAAAGGACGATATACGGGTGAACCGTTAAGAGAGCGCCCTCAATGTC	1860
Db	6298	TGTAGATGACAAAGGACGATATACGGGTGAACCGTTAAGAGAGCGCCCTCAATGTC	6357
Qy	1861	GAGCGGCTTCAACCTCGTTCTACCGCTTACCGCAACAGTCTCAATCATGAC	1920
Db	6358	GAGCGGCTTCAACCTCGTTCTACCGCTTACCGCAACAGTCTCAATCATGAC	6417
Qy	1921	CGCGCCCTTAGCCAAAGTTGGTTAGAGAAATGATGAAAGAGAGCAAAAAATACATGGCG	1980
Db	6418	CGCGCCCTTAGCCAAAGTTGGTTAGAGAAATGATGAAAGAGAGCAAAAAATACATGGCG	6477
Qy	1981	TTGATATTCGGGATTCGAATCTTTATCTTAAAGTAGTAGGCTTGGCTATATCTGTAGCC	2040

Db 6478 |||||TTGATAATCCGGATTGCAATCTTATTCTTAACAGTAGTGACTTGGCTATATCTGTAGCC 6537
Qy 2041 TCCCTTTTATATAGCATGGGGCTAGCACCTTAGCGATCTTGTAGGCATACCGACTAGG 2100
Db 6538 TCCCTTTTATATAGCATGGGGCTAGCACCTTAGCGATCTTGTAGGCATACCGACTAGG 6597
Qy 2101 ATTTCCAGGGCAGAAAGAAAGATTACATCTACACTCTGGTTCCAAATCAAGATGTAGTAGAT 2160
Db 6598 ATTTCCAGGGCAGAAAGAAAGATTACATCTACACTCTGGTTCCAAATCAAGATGTAGTAGAT 6657
Qy 2161 AGGATATATAAGCAAGTGGCCCTTGAGTCTCCGTTGGCATTTGTTAAATATCTGAGACAACA 2220
Db 6658 AGGATATATAAGCAAGTGGCCCTTGAGTCTCCGTTGGCATTTGTTAAATATCTGAGACAACA 6717
Qy 2221 ATTATGAACCAATAACATCTCTCTTATCAGATTAATGGAGCTGCAAAACACAGTGGG 2280
Db 6718 ATTATGAACCAATAACATCTCTCTTATCAGATTAATGGAGCTGCAAAACACAGTGGG 6777
Qy 2281 TGGGGGGCACCCTATCCATGACCCAGATTATATAGGGGGGATAGGCAAAAGAACTCATTTGTA 2340
Db 6778 TGGGGGGCACCCTATCCATGACCCAGATTATAGGGGGGATAGGCAAAAGAACTCATTTGTA 6837
Qy 2341 GATGATCTAGTGTGATCAATCATTTCTATCCCTCTGCATTTCAAGAAACATCTGAATTTT 2400
Db 6838 GATGATCTAGTGTGATCAATCATTTCTATCCCTCTGCATTTCAAGAAACATCTGAATTTT 6897
Qy 2401 ATCCCGGGCTACTACAGGATCAGGTTGCACTCGAATACCCCTATTGTGACATGAGTCT 2460
Db 6898 ATCCCGGGCTACTACAGGATCAGGTTGCACTCGAATACCCCTATTGTGACATGAGTCT 6957
Qy 2461 ACCCATTTACTGCTACACCCCAATATGTAATTTGTCGATGTCAGAGATCACTCACATTCA 2520
Db 6958 ACCCATTTACTGCTACACCCCAATATGTAATTTGTCGATGTCAGAGATCACTCACATTCA 7017
Qy 2521 TATCAGTATTTAGCACTTGGTGTCTCCGGACATCTGCAACAGGGAGGGTATTCTTTTCT 2580
Db 7018 TATCAGTATTTAGCACTTGGTGTCTCCGGACATCTGCAACAGGGAGGGTATTCTTTTCT 7077
Qy 2581 ACTCTGGGTTCCATCAACCTGGACGACACCCAAATCGGAAGTCTTCAGTGTAGTGCA 2640
Db 7078 ACTCTGGGTTCCATCAACCTGGACGACACCCAAATCGGAAGTCTTCAGTGTAGTGCA 7137
Qy 2641 ACTCCCTCGGTTGTGATATGCTGTCTCGAAAGTCAAGAGTCAAGAGGAAGAAATTAT 2700
Db 7138 ACTCCCTCGGTTGTGATATGCTGTCTCGAAAGTCAAGAGTCAAGAGGAAGAAATTAT 7197
Qy 2701 AACTCAGCTGTCCCTACCGGATGGTACATGGGAGGTTAGGGTTTCGACGGCCAGTACCAC 2760
Db 7198 AACTCAGCTGTCCCTACCGGATGGTACATGGGAGGTTAGGGTTTCGACGGCCAGTACCAC 7257
Qy 2761 GAAAAGGACCTAGATGTCAACAATTTATTCGGGACCTGGGTGGCCAACTACCCAGGATTA 2820
Db 7258 GAAAAGGACCTAGATGTCAACAATTTATTCGGGACCTGGGTGGCCAACTACCCAGGATTA 7317
Qy 2821 GGGGTTGGATCTTTTATTGACAGCCGGTATGTTCTCAGTCTACGGAGGGTTAAACCC 2880
Db 7318 GGGGTTGGATCTTTTATTGACAGCCGGTATGTTCTCAGTCTACGGAGGGTTAAACCC 7377
Qy 2881 AATTCAACCCAGTGCACCTGTACAGGAAGGGAATATGTGATATACAAGCGATACAATGAC 2940
Db 7378 AATTCAACCCAGTGCACCTGTACAGGAAGGGAATATGTGATATACAAGCGATACAATGAC 7437
Qy 2941 ACATGCCAGATGAGCAAGACTACAGATTCGAATGGCCAAAGTCTTCGTATAGCCCTGGA 3000
Db 7438 ACATGCCAGATGAGCAAGACTACAGATTCGAATGGCCAAAGTCTTCGTATAGCCCTGGA 7497
Qy 3001 CGGTTTGTGGAAACCATACACAGCAGCTATCTTATCTCAAGGTGTCAACATCCTTA 3060
Db 7498 CGGTTTGTGGAAACCATACACAGCAGCTATCTTATCTCAAGGTGTCAACATCCTTA 7557
Qy 3061 GGGGAAGACCCGGTATCTGACTGTATCCGCCCAACACAGTCACTCATGTGGGGCCGAAGGC 3120
Db |||||

Db 7558 GGGGAAGACCCGGTACTGACTGTATCCGCCCAACACAGTCACTCAATGGGGCCGAAGGC 7617
Qy 3121 AGAATTTCTACAGTAGGGACATCTCATTTTCTTGTATCAACGAGGGTCACTCATCTTCTCT 3180
Db 7618 AGAATTTCTACAGTAGGGACATCTCATTTTCTTGTATCAACGAGGGTCACTCATCTTCTCT 7677
Qy 3181 CCGCGCTTATTATATCTTATGACAGTCAAGCAACAAACAGCCACTTTTCATAGTCTTAT 3240
Db 7678 CCGCGCTTATTATATCTTATGACAGTCAAGCAACAAACAGCCACTTTTCATAGTCTTAT 7737
Qy 3241 ACATTTCAATGCTTCACTCGGCCAGGTAGTATCCCTTGGCAGGCTTCAGCAAGATGCCCC 3300
Db 7738 ACATTTCAATGCTTCACTCGGCCAGGTAGTATCCCTTGGCAGGCTTCAGCAAGATGCCCC 7797
Qy 3301 AACTCGTGTGTTACTCGAGTCTATACAGATCCATATCCCTATCTTCTATAGAAACC 3358
Db 7798 AACTCGTGTGTTACTCGAGTCTATACAGATCCATATCCCTATCTTCTATAGAAACC 7855
RESULT 5
US-10-824-782-134
; Sequence 134, Application US/10824782
; Publication No. US20040234552A1
; GENERAL INFORMATION:
; APPLICANT: Peeters, Bernadus; de Leeuw, Olav; Klaus, Guus; Gielkens, Arnold
; TITLE OF INVENTION: Newcastle Disease Virus Infectious Clones, Vaccines and Diagnostic
; FILE REFERENCE: 2183-4646US
; CURRENT APPLICATION NUMBER: US/10/824,782
; CURRENT FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: US/10/788,232
; PRIOR FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: PCT/NL99/00377
; PRIOR FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 134
; LENGTH: 15186
; TYPE: DNA
; ORGANISM: Newcastle disease virus strain LaSota
US-10-824-782-134
Query Match 99.9%; Score 3353.2; DB 20; Length 15186;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3355; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 ACGGGTAGAGATTCTGGATCCCGGTTGGCGCCCTCCAGGTGCAAGTGGGCTCCAGACC 60
Db 4498 ACGGGTAGAAGATTCTGGATCCCGGTTGGCGCCCTCCAGGTGCAAGTGGGCTCCAGACC 4557
Qy 61 TTCTACAAAGAACCCAGCACCTATGATGCTGACTATCCGGTTGCGTGGCACTGAGTTG 120
Db 4558 TTCTACAAAGAACCCAGCACCTATGATGCTGACTATCCGGTTGCGTGGTACTGAGTTG 4617
Qy 121 CATTCTGTCGGGCAAACTCCAATTGATGCGCAGGCTCTTTGACGTGCGAGGAATTTGGTTAC 180
Db 4618 CATTCTGTCGGGCAAACTCCAATTGATGCGCAGGCTCTTTGACGTGCGAGGAATTTGGTTAC 4677
Qy 181 AGGAGACAAAGCCGTCACATATACACCTCATCCGACAGGATCAATCATAGTTAAGCT 240
Db 4678 AGGAGACAAAGCCGTCACATATACACCTCATCCGACAGGATCAATCATAGTTAAGCT 4737
Qy 241 CTTCCCGAATCTCCCAAGGATTAAGAGGATGTCGAAAGCCCTTGGATGCATACAA 300
Db 4738 CTTCCCGAATCTCCCAAGGATTAAGAGGATGTCGAAAGCCCTTGGATGCATACAA 4797
Qy 301 CAGGACATTGACCACTTTGCTCAACCCCTTGGTGACTCTATCCGTAGGATACAAGATC 360
Db 4798 CAGGACATTGACCACTTTGCTCAACCCCTTGGTGACTCTATCCGTAGGATACAAGATC 4857
Qy 361 TGTGACTACATCTGGAGGGGGAGACAGGGGCGCTTATAGGCGCCATTTATGGCGGTGT 420
Db 4858 TGTGACTACATCTGGAGGGGGAGACAGGGGCGCTTATAGGCGCCATTTATGGCGGTGT 4917

QY 421 GCCTCTTGGGGTTGCAACTGCCGCAAAATACAGCGCGCGAGCTCTGTATCAAGCCAA 480
DB 4918 GCCTCTTGGGGTTGCAACTGCCGCAAAATACAGCGCGCGAGCTCTGTATCAAGCCAA 4977
QY 481 ACAAAATGCTGCAACATCTCTCCGACTTAAAGAGAGCAATGCGCAACCAATGAGGCTGT 540
DB 4978 ACNAAATGCTGCCAACAATCTCTCCGACTTAAAGAGAGCAATGCGCAACCAATGAGGCTGT 5037
QY 541 GCATGAGTCACTGACCGGATTATCGCAACTAGCAGTGGCAGTTGGGAAGATGCAAGCAGTT 600
DB 5038 GCATGAGTCACTGACCGGATTATCGCAACTAGCAGTGGCAGTTGGGAAGATGCAAGCAGTT 5097
QY 601 TGTAAATGACCAATTTAATAAAGCTCAGGAATTTAGACTGCATCAAAAATGCAACAGCA 660
DB 5098 TGTAAATGACCAATTTAATAAAGCTCAGGAATTTAGACTGCATCAAAAATGCAACAGCA 5157
QY 661 AGTTGGTGTAGAGCTCAACCTGTACTTAACCGAATTTAGACTCAGTATTTCCGACCAACAAT 720
DB 5158 AGTTGGTGTAGAGCTCAACCTGTACTTAACCGAATTTAGACTCAGTATTTCCGACCAACAAT 5217
QY 721 CACTTCACCTGCTTTAAACAAGCTGACTATTTCAGGCACTTTTACAACTTAGCTGTGGAAA 780
DB 5218 CACTTCACCTGCTTTAAACAAGCTGACTATTTCAGGCACTTTTACAACTTAGCTGTGGAAA 5277
QY 781 TATGGATTACTATTATGACTAAGTTAGGTAGGGAACAATCAACTCAGCTCATTAATCGG 840
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QY 841 TAGGGCTTAATCACCGGTAAACCTTATCTATACGACTCACAGACTCAACTCTTGGGTAT 900
DB 5338 TAGGGCTTAATCACCGGTAAACCTTATCTATACGACTCACAGACTCAACTCTTGGGTAT 5397
QY 901 ACAGTAACTCTACCTTCAGTCCGGAACCTTAAATAATATGGTGGCCACTACTTTGGAAAC 960
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DB 5518 GGTGGTTCGTGATAGAAAGTCTGACACCTCATACCTGATAGAAAGTCTAGATTT 5577
QY 1081 ATATTGTACAAAGATAGTAAAGTTCCTTATGTCCCTGCTGATTTATTCCTGCTGAGCGG 1140
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DB 5638 CAATACGTGGCTGTATGTACTCAAGACCGAAGCGGCACTTACTACCAATACATGAC 5697
QY 1201 TATCAAGGTTTCAGTCATCGCCACTGCAAGATGACACATGTAGATGTGTAACCCCCC 1260
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QY 1261 GGGTATCATATCGCAAAATATGGAAGACCGTGTCTCTAATAGATAAACAATCATGCAA 1320
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QY 1321 TGTTTTATCTTAGCGGGATAAATTTTAAAGGCTCAGTGGGAAATTCGATGTAACTTATCA 1380
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DB 5938 TGAGCTTGGGAATGTCAACAACCTCGATCAGTAAATGCTTTGAATAGTTAGAGGAAGCAA 5997
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DB 5998 CAGAAAACCTAGACAAAGTCAATGTCAAACTGACTAGCACATCTGCTCTCATTTACCTATAT 6057
QY 1561 CGTTTTCAGTATCATATCTCTTGTGTTTGGTATATCTTAGCCTGTATTTAGCATGTACCT 1620
DB 6058 CGTTTTCAGTATCATATCTCTTGTGTTTGGTATATCTTAGCCTGTATTTAGCATGTACCT 6117
QY 1621 AATGTACAGCAAAAGGCGCAACAAAAACCTTATTTATGGCTTGGGAATAATATCTCTAGA 1680
DB 6118 AATGTACAGCAAAAGGCGCAACAAAAACCTTATTTATGGCTTGGGAATAATATCTCTAGA 6177
QY 1681 TCAGATGAGGCCACTACAAAAATGTGAACACAGATGAGAAACGAAGGTTTCCCTTAATAG 1740
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QY 1741 TAAATTTGTGTAAGAGTTCTGCTAGTCTGTCTAGTTCAGAGGTTTAAAGAAAAAATACCCGT 1800
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QY 1801 TGTAGATGACCAAAAGGAGATATACGGGTAGAAACGGTAAAGAGAGCCGCCCTCAATTGC 1860
DB 6298 TGTAGATGACCAAAAGGAGATATACGGGTAGAAACGGTAAAGAGAGCCGCCCTCAATTGC 6357
QY 1861 GAGCCAGCTTTCACAACTCCGTTCTACCGCTTCCACGACAAACAGTCTCAATCATGAC 1920
DB 6358 GAGCCAGCTTTCACAACTCCGTTCTACCGCTTCCACGACAAACAGTCTCAATCATGAC 6417
QY 1921 CGCCCGCTTAGCCAAAGTTGCGTTAGAGAAATGATGAAAGAGAGGCAAAAAATACATGGCGC 1980
DB 6418 CGCCCGCTTAGCCAAAGTTGCGTTAGAGAAATGATGAAAGAGAGGCAAAAAATACATGGCGC 6477
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QY 2041 TCCCTTTTATATAGCATGGGGCTAGCACACTAGCGATCTTGTAGGCATACCGACTAGG 2100
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QY 2101 ATTTCCAGGGCAGAAAGAAAGATTACATCTACACTTGGTTCCTTCAAGATGTAGTAGAT 2160
DB 6598 ATTTCCAGGGCAGAAAGAAAGATTACATCTACACTTGGTTCCTTCAAGATGTAGTAGAT 6657
QY 2161 AGGATATATAAGCAAGTGGCCCTTGGCTCCGTTGGCAATTTGTTAAATATCTGAGACCACA 2220
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QY 2221 ATTTAGAACGCAATTAACATCTCTCTTATCAGATTAATGAGCTTGCAAAACAAAGTGGG 2280
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QY 2461 ACCCATTTACTGCTACACCCCAATATGTAATTTGTCTGATGTCAGAGATCACTCAATTTCA 2520
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DB 7018 TATCAGTATTTAGCACTTGGTGTCTCGGACATCTGCAACAGGGAGGGTATTTCTTTCT 7077
QY 2581 ACTCTGGCTTCCATCAACCTGGAACGACCCCAAAATCGGAAGTCTTGCAAGTGTGAGTGCA 2640

Db	7078	ACTCTGCGTTCCATCAACCTGGACACACCCAAATAATCGGAAGTCTTGGCAGTGTGAGTGCA	7137
Qy	2641	ACTCCCCCTGGTGTGTATATGCTGTGCTCGAAAGTACACGAGACAGAGGAAGAAGATTAT	2700
Db	7138	ACTCCCCCTGGTGTGTATATGCTGTGCTCGAAAGTACACGAGACAGAGGAAGAAGATTAT	7197
Qy	2701	AATCTCAGCTGTCCCTACCGCGATGGTATACATGGGAGGTTAGGGTTTCGACGGCCAGTACCAC	2760
Db	7198	AATCTCAGCTGTCCCTACCGCGATGGTATACATGGGAGGTTAGGGTTTCGACGGCCAGTACCAC	7257
Qy	2761	GAAGAAGACCTAGATGTCAACAATATTTCCGGGACCTGGGTGGCAACTACCCAGAGTA	2820
Db	7258	GAAGAAGACCTAGATGTCAACAATATTTCCGGGACCTGGGTGGCAACTACCCAGAGTA	7317
Qy	2821	GGGGTGGATCTTTATTTGACAGCCGCTATGGTTCTCAGTCTACGAGGGTTTAAACCC	2880
Db	7318	GGGGTGGATCTTTATTTGACAGCCGCTATGGTTCTCAGTCTACGAGGGTTTAAACCC	7377
Qy	2881	AATTCACCCAGTGACACTGTACAGGAAGGAAATATGTGATATACAAAGCGATACAATGAC	2940
Db	7378	AATTCACCCAGTGACACTGTACAGGAAGGAAATATGTGATATACAAAGCGATACAATGAC	7437
Qy	2941	ACATGCCAGATGAGCAAGTACACAGATTTCGAATGGCCAAAGTCTTCGTATAGCCCTGGA	3000
Db	7438	ACATGCCAGATGAGCAAGTACACAGATTTCGAATGGCCAAAGTCTTCGTATAGCCCTGGA	7497
Qy	3001	CGGTTTGGTGGGAAACSCATACAGCAGGCTATCTTATCTATCAAGGTGTCAACATCCTTA	3060
Db	7498	CGGTTTGGTGGGAAACSCATACAGCAGGCTATCTTATCTATCAAGGTGTCAACATCCTTA	7557
Qy	3061	GGCGAAGACCCGGTACTGACTGTACCGCCCAACAACAGTCACTCATGTGGGGCCGAAGGC	3120
Db	7558	GGCGAAGACCCGGTACTGACTGTACCGCCCAACAACAGTCACTCATGTGGGGCCGAAGGC	7617
Qy	3121	AGAAATTCACAGTAGGGAATCTCATTTCTTGTTATCAACAGAGGTCACTATCTCT	3180
Db	7618	AGAAATTCACAGTAGGGAATCTCATTTCTTGTTATCAACAGAGGTCACTATCTCT	7677
Qy	3181	CCGCGTTATTATATCTTATGACAGTCAAGCAACAAACAGCCACTCTTCATAGTCTCTAT	3240
Db	7678	CCGCGTTATTATATCTTATGACAGTCAAGCAACAAACAGCCACTCTTCATAGTCTCTAT	7737
Qy	3241	ACATTCATAGTCCCTTCACTCGCCAGGTAGTATCCCTTTCGAGGCTTCAGCAAGATGCCCC	3300
Db	7738	ACATTCATAGTCCCTTCACTCGCCAGGTAGTATCCCTTTCGAGGCTTCAGCAAGATGCCCC	7797
Qy	3301	AATCGTGTGTACTGAGTCTATACAGATCCATATCCCTTAATCTTCTATAGAAACC	3358
Db	7798	AATCGTGTGTACTGAGTCTATACAGATCCATATCCCTTAATCTTCTATAGAAACC	7855

RESULT 6
US-10-788-232-134
; Sequence 134, Application US/10788232
; Publication No. US20040235134A1
; GENERAL INFORMATION:
; APPLICANT: Peeters, Bernardus; de Leeuw, Olav; Klaus, Guus; Gielkens, Arnold
; TITLE OF INVENTION: Newcastle Disease Virus Infectious Clones, Vaccines and Diagnostic
; FILE REFERENCE: 2183-4646US
; CURRENT APPLICATION NUMBER: US/10/788,232
; CURRENT FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: PCT/NL99/00377
; PRIOR FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 134
; LENGTH: 15186
; TYPE: DNA
; ORGANISM: Newcastle disease virus strain LaSota
US-10-788-232-134

Query Match 99.9%; Score 3353.2; DB 20; Length 15186;
Best Local Similarity 99.9%; Pred. No. 0;

		Matches 3355; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	
Qy	1	ACGGGTAGAAAGATTCTTGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGCTCCAGACC	60
Db	4498	ACGGGTAGAAAGATTCTTGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGCTCCAGACC	4557
Qy	61	TTCTACCAAGAACCCAGCACCTATGATGTGACTATCCGGGTTGCGCTGGCACTGAGTTG	120
Db	4558	TTCTACCAAGAACCCAGCACCTATGATGTGACTATCCGGGTTGCGCTGGCACTGAGTTG	4617
Qy	121	CATCTGTCCGGCAAACTCCATTGATGGCAGGCTCTTTCAGCTGCGAGGAATTTGCTGTAC	180
Db	4618	CATCTGTCCGGCAAACTCCATTGATGGCAGGCTCTTTCAGCTGCGAGGAATTTGCTGTAC	4677
Qy	181	AGGAGACAAAGCGCTCAACATATACACCTCATCCACAGACAGGATCAATCATAGCTTAAGCT	240
Db	4678	AGGAGACAAAGCGCTCAACATATACACCTCATCCACAGACAGGATCAATCATAGCTTAAGCT	4737
Qy	241	CCTCCCGAATCTGCCCAAGGATAAGGAGCATGTGCGAAAGCCCTTTCGATGCATACAA	300
Db	4738	CCTCCCGAATCTGCCCAAGGATAAGGAGCATGTGCGAAAGCCCTTTCGATGCATACAA	4797
Qy	301	CAGGACATTTGACCACTTTGCTCACCCCCTTGGTGACTCTATCCGTAGGATACAAAGTTC	360
Db	4798	CAGGACATTTGACCACTTTGCTCACCCCCTTGGTGACTCTATCCGTAGGATACAAAGTTC	4857
Qy	361	TGTGACTTACATCTGGAGGGGGAGACAGGGGCCCTTATAGGGCCCAATTTATGGCCGTGT	420
Db	4858	TGTGACTTACATCTGGAGGGGGAGACAGGGGCCCTTATAGGGCCCAATTTATGGCCGTGT	4917
Qy	421	GGCTCTTGGGTTGCAACTTCCCGCACAAAATAACAGCGCGCGAGCTCTGANTACAAAGCCAA	480
Db	4918	GGCTCTTGGGTTGCAACTTCCCGCACAAAATAACAGCGCGCGAGCTCTGANTACAAAGCCAA	4977
Qy	481	ACAAATGTCCCAACATCTCCGACTTAAAGAGACATTTGCCGCAACCAATGAGGCTGT	540
Db	4978	ACAAATGTCCCAACATCTCCGACTTAAAGAGACATTTGCCGCAACCAATGAGGCTGT	5037
Qy	541	GCATGAGTCACTGACGGATTATCGCAACTAGCAGTGGCAGTTGGGAAGATGACAGAGTT	600
Db	5038	GCATGAGTCACTGACGGATTATCGCAACTAGCAGTGGCAGTTGGGAAGATGACAGAGTT	5097
Qy	601	TGTTAATGACCAATTTAATAAAACAGCTCAGGAATTAGATCGATCAAAATTCACAGCA	660
Db	5098	TGTTAATGACCAATTTAATAAAACAGCTCAGGAATTAGATCGATCAAAATTCACAGCA	5157
Qy	661	AGTTGTTGATAGCTCAACCTGTACCTAACCGAATTTGACTACAGTATTCGACCACAAAAT	720
Db	5158	AGTTGTTGATAGCTCAACCTGTACCTAACCGAATTTGACTACAGTATTCGACCACAAAAT	5217
Qy	721	CACCTCACCTGCTTTAAACAAAGCTGACTATTTCAGGCACCTTTTCAATCTAGCTGGTGA	780
Db	5218	CACCTCACCTGCTTTAAACAAAGCTGACTATTTCAGGCACCTTTTCAATCTAGCTGGTGA	5277
Qy	781	TATGATTACTTATTGACTAAGTTAGGTGTAGGGAACAATCAACTCAGCTCATTAATCGG	840
Db	5278	TATGATTACTTATTGACTAAGTTAGGTGTAGGGAACAATCAACTCAGCTCATTAATCGG	5337
Qy	841	TAGCGGCTTAATCACCAGTAAACCTATTCTATACGACTACAGACTCAACTCTTTGGGTAT	900
Db	5338	TAGCGGCTTAATCACCAGTAAACCTATTCTATACGACTACAGACTCAACTCTTTGGGTAT	5397
Qy	901	ACAGGTAACTCTACCTTTCAGTCCGGGAACCTTAAATAATATATCGGTGCCACCTACTTGA	960
Db	5398	ACAGGTAACTCTACCTTTCAGTCCGGGAACCTTAAATAATATATCGGTGCCACCTACTTGA	5457
Qy	961	CTTATCCGTAAGCAACAACGAGGGAATTTGCCTCGGCACTTGTCCCAAAAGTGTGACACA	1020
Db	5458	CTTATCCGTAAGCAACAACGAGGGAATTTGCCTCGGCACTTGTCCCAAAAGTGTGACACA	5517
Qy	1021	GGTCCGTTCTGTGATAGAGAACTTACACCTCATACTGTATAGAAAGTACTTAGATTTT	1080
Db	5518	GGTCCGTTCTGTGATAGAGAACTTACACCTCATACTGTATAGAAAGTACTTAGATTTT	5577

Qy	1081	ATATTGTAAGAATAGTAACGTTCCCTTATGTCCCTGGTATTTATTCCTGCTTGAGGG	1140
Db	5578	ATAATTGTAAGAATAAGTAACGTTCCCTTATGTCCCTGGTATTTATTCCTGCTTGAGGG	5637
Qy	1141	CAATAAGTCCGCTGTATGTACTCAAGACCGAAGCGCACTTACTACACATACATGAC	1200
Db	5638	CAATAAGTCCGCTGTATGTACTCAAGACCGAAGCGCACTTACTACACATACATGAC	5697
Qy	1201	TATCAAAAGTTTCAGTCATCGCAACTGCAAGATGACAAATGTAGATGTGTAACCCGCC	1260
Db	5698	TATCAAAAGTTTCAGTCATCGCAACTGCAAGATGACAAATGTAGATGTGTAACCCGCC	5757
Qy	1261	GGGTATCATATCGCAAAACTATGAGAAAGCCGTGTCTCTATAGATAAACAATCATGCAA	1320
Db	5758	GGGTATCATATCGCAAAACTATGAGAAAGCCGTGTCTCTATAGATAAACAATCATGCAA	5817
Qy	1321	TGTTTATTCCTTAGCGGGATAAATTTAAAGCTCAGTGGGGAATTCGATGTAACTTATCA	1380
Db	5818	TGTTTATTCCTTAGCGGGATAAATTTAAAGCTCAGTGGGGAATTCGATGTAACTTATCA	5877
Qy	1381	GAAGAATATCTCAATACAAAGATCTCTCAAGTAAATAAACAAGCAATCTTGATATCTCAAC	1440
Db	5878	GAAGAATATCTCAATACAAAGATCTCTCAAGTAAATAAACAAGCAATCTTGATATCTCAAC	5937
Qy	1441	TGAGCTTGGGAATGTCAACAACTCGATCAGTAAATGCTTTTGAATTAAGTTAGAGGAAGCAA	1500
Db	5938	TGAGCTTGGGAATGTCAACAACTCGATCAGTAAATGCTTTTGAATTAAGTTAGAGGAAGCAA	5997
Qy	1501	CAGAAACTAGCAAAAGTCAATGTCAAACTGACTAGCAATCTGCTCTCATTAACCTATAT	1560
Db	5998	CAGAAACTAGCAAAAGTCAATGTCAAACTGACTAGCAATCTGCTCTCATTAACCTATAT	6057
Qy	1561	CGTTTGAATATCATATCTCTTGTGTTTGGTATATCTAGCCCTGATCTTAGCATGCTACCT	1620
Db	6058	CGTTTGAATATCATATCTCTTGTGTTTGGTATATCTAGCCCTGATCTTAGCATGCTACCT	6117
Qy	1621	AATGTACAAAGGCGCAACAAAAAACCCTTATATGCTTGGTAAATAATATCTCTAGA	1680
Db	6118	AATGTACAAAGGCGCAACAAAAAACCCTTATATGCTTGGTAAATAATATCTCTAGA	6177
Qy	1681	TCAGATGAGCCACTACAAAATGTGAACACAGATGAGGAACGAAGTTTCCCTAATAG	1740
Db	6178	TCAGATGAGCCACTACAAAATGTGAACACAGATGAGGAACGAAGTTTCCCTAATAG	6237
Qy	1741	TAAATTGTGTGAAGTTCTGCTAGTCTCTCAGTTCAGAGAGTTAAGAAAAAATACCGGT	1800
Db	6238	TAAATTGTGTGAAGTTCTGCTAGTCTCTCAGTTCAGAGAGTTAAGAAAAAATACCGGT	6297
Qy	1801	TGTAGATGACCAAGGACGATATACGGGTAGAACGTTAAGAGAGGCCGCCCTCAATTGC	1860
Db	6298	TGTAGATGACCAAGGACGATATACGGGTAGAACGTTAAGAGAGGCCGCCCTCAATTGC	6357
Qy	1861	GAGCAGGCTTCACAACTCCGTTCTACCGTTCACCGACAAAGTCTCAATCATGGAC	1920
Db	6358	GAGCAGGCTTCACAACTCCGTTCTACCGTTCACCGACAAAGTCTCAATCATGGAC	6417
Qy	1921	CGCGCGTTAGCCAAAGTTGCGTTAGAGAAATCGAAGAGAGGCAAAAAATACATGGCG	1980
Db	6418	CGCGCGTTAGCCAAAGTTGCGTTAGAGAAATCGAAGAGAGGCAAAAAATACATGGCG	6477
Qy	1981	TTGATATTCGGATTTGCAATCTTATTTTAAACAGTAGTGACCTTGGCTATATCTGTAGCC	2040
Db	6478	TTGATATTCGGATTTGCAATCTTATTTTAAACAGTAGTGACCTTGGCTATATCTGTAGCC	6537
Qy	2041	TCCCTTTTATATAGCATGGGGCTAGCACACTAGCGATCTTTGAGGCATACCGACTAGG	2100
Db	6538	TCCCTTTTATATAGCATGGGGCTAGCACACTAGCGATCTTTGAGGCATACCGACTAGG	6597
Qy	2101	ATTTCCAGGCGAGAAAGATTAATCTACATCTGGTTCCAAATCAAGATGTAGTAGAT	2160
Db	6598	ATTTCCAGGCGAGAAAGATTAATCTACATCTGGTTCCAAATCAAGATGTAGTAGAT	6657

Qy	2161	AGGATATATAAGCAAGTGGCCCTTGAGTCTCCGTTGGCATTTGTTAAATFACATGAGACACA	2220
Db	6658	AGGATATATAAGCAAGTGGCCCTTGAGTCTCCGTTGGCATTTGTTAAATFACATGAGACACA	6717
Qy	2221	ATTATGAACGCAATAAATCATCTCTCTTATCAGATTAATGGAGCTGCAAAACAAGTGGG	2280
Db	6718	ATTATGAACGCAATAAATCATCTCTCTTATCAGATTAATGGAGCTGCAAAACAAGTGGG	6777
Qy	2281	TGGGGGACCTATTCATGACCCAGATATATATAGGGGGATAGGCAAAAGAACTCATTTGTA	2340
Db	6778	TGGGGGACCTATTCATGACCCAGATATATATAGGGGGATAGGCAAAAGAACTCATTTGTA	6837
Qy	2341	GATCATGCTAGTGATGTCACATCATCTTATCCCTCTCATTTTCAAGAACTCTGAAATTTT	2400
Db	6838	GATCATGCTAGTGATGTCACATCATCTTATCCCTCTCATTTTCAAGAACTCTGAAATTTT	6897
Qy	2401	ATCCCGCGGCTACTACAGGATCAGGTTGCACTCGAATACCCCTCATTTTGAATGAGTGCT	2460
Db	6898	ATCCCGCGGCTACTACAGGATCAGGTTGCACTCGAATACCCCTCATTTTGAATGAGTGCT	6957
Qy	2461	ACCATTTACTGCTACACCCATAATGTAATATTTGTCTGGATGCGAGATCACTCAATTCA	2520
Db	6958	ACCATTTACTGCTACACCCATAATGTAATATTTGTCTGGATGCGAGATCACTCAATTCA	7017
Qy	2521	TATCAGTATTTAGCACTTGGTGTCTCGGACATCTGCAACAGGAGGTTATTTCTTCT	2580
Db	7018	TATCAGTATTTAGCACTTGGTGTCTCGGACATCTGCAACAGGAGGTTATTTCTTCT	7077
Qy	2581	ACTCTGGGTTCCATCAACCTGGACGACACCCAAATCGGAAGTCTTGCAGTGTGAGTGCA	2640
Db	7078	ACTCTGGGTTCCATCAACCTGGACGACACCCAAATCGGAAGTCTTGCAGTGTGAGTGCA	7137
Qy	2641	ACTCCCCTGGGTTGTGATATGCTGTCTCGAAAGTACCGGAGACAGAGGAAGAAGATTAT	2700
Db	7138	ACTCCCCTGGGTTGTGATATGCTGTCTCGAAAGTACCGGAGACAGAGGAAGAAGATTAT	7197
Qy	2701	AACCTCAGTGTCCCTACCGGATGGTACATGGGAGTTAGGTTTCGACGGCCAGTACCAC	2760
Db	7198	AACCTCAGTGTCCCTACCGGATGGTACATGGGAGTTAGGTTTCGACGGCCAGTACCAC	7257
Qy	2761	GAAGAAGACCTAGATGTCAAAATTTATCGGGACCTGGGTGGCCAACTACCCAGGAGTA	2820
Db	7258	GAAGAAGACCTAGATGTCAAAATTTATCGGGACCTGGGTGGCCAACTACCCAGGAGTA	7317
Qy	2821	GGGGTGGATCTTTTATTTGAACGCGGTATGGTTCTCAGTCTACGAGGGTTAAAAACC	2880
Db	7318	GGGGTGGATCTTTTATTTGAACGCGGTATGGTTCTCAGTCTACGAGGGTTAAAAACC	7377
Qy	2881	AATTCAACCGATGACCTGTACAGGAAGGAAATATGTGATATACAGCGATACATGAC	2940
Db	7378	AATTCAACCGATGACCTGTACAGGAAGGAAATATGTGATATACAGCGATACATGAC	7437
Qy	2941	ACATGCCAGATGAGCAAGACTACAGATTTCGAATGGCCAGTCTTCGTATAAGCCTGGA	3000
Db	7438	ACATGCCAGATGAGCAAGACTACAGATTTCGAATGGCCAGTCTTCGTATAAGCCTGGA	7497
Qy	3001	CGGTTTGGTGGAAAACGCATACAGCAGGCTATCTTATCTATCAAGGTGTCAACATCTT	3060
Db	7498	CGGTTTGGTGGAAAACGCATACAGCAGGCTATCTTATCTATCAAGGTGTCAACATCTT	7557
Qy	3061	GGCGAAGACCGGTTACTGACTGTAACCGCCAAACAGTCACTCATGCGGGGGCGAAGGC	3120
Db	7558	GGCGAAGACCGGTTACTGACTGTAACCGCCAAACAGTCACTCATGCGGGGGCGAAGGC	7617
Qy	3121	AGATTCTCAGTAGGACATCTCATTTCTTGTATCAACGAGGTCTATCATCTCTCT	3180
Db	7618	AGATTCTCAGTAGGACATCTCATTTCTTGTATCAACGAGGTCTATCATCTCTCTCT	7677
Qy	3181	CCCCGGTTATTTATATCTTATGACAGTCAAGCAAAAAACAGCCACTCTTTCATAGTCTTAT	3240
Db	7678	CCCCGGTTATTTATATCTTATGACAGTCAAGCAAAAAACAGCCACTCTTTCATAGTCTTAT	7737
Qy	3241	ACATTCAATGCCTTCACTCGGCCAGGTAGTATCCCTTCCAGGCTTCAGCAAGATGCCCC	3300


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Db 7738 ACATTCAATGCTTCACTCGCCAGGTAGTATCCCTTGCAGGCTTCAGCAAGATGCCCC 7797
Qy 3301 AACTCGTGTCTACTGAGTCTATACAGATCCATATCCCTAATCTTCTATAGAAACC 3358
Db 7798 AACTCGTGTCTACTGAGTCTATACAGATCCATATCCCTAATCTTCTATAGAAACC 7855

RESULT 7
US-10-440-419-55
; Sequence 55, Application US/10440419
; Publication No. US20030224017A1
; GENERAL INFORMATION:
; APPLICANT: SAMAL, SIBA K.
; APPLICANT: HUANG, ZHUHUI
; TITLE OF INVENTION: RECOMBINANT NEWCASTLE DISEASE VIRUSES USEFUL AS
; FILE OF INVENTION: VACCINES OR VACCINE VECTORS
; FILE REFERENCE: 108172-00096
; CURRENT APPLICATION NUMBER: US/10/440,419
; CURRENT FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: 09/926,431
; PRIOR FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: PCT/US00/06700
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/381,462
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/171,072
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: 60/132,597
; PRIOR FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 15900
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Recombinant cDNA for NDV
US-10-440-419-55

Query Match 99.7%; Score 3346.8; DB 17; Length 15900;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 3351; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ACGGTTAGAGATTCTGGATCCGGTTGGCGCCCTCCAGGTGCAAGATGGCTCCAGACC 60
Db 5212 ACGGTTAGAGATTCTGGATCCGGTTGGCGCCCTCCAGGTGCAAGATGGCTCCAGACC 5271

Qy 61 TTCTACCAAGAACCCAGCACTATGATGCTGACTATCCGGGTTGCGCTGGCACTGAGTTG 120
Db 5272 TTCTACCAAGAACCCAGCACTATGATGCTGACTATCCGGGTTGCGCTGGCACTGAGTTG 5331

Qy 121 CATCTGTCGGGCAAACTCCATTGATGAGCGAGCCCTCTTGACAGCTGCGAGGAATTGGGTTAC 180
Db 5332 CATCTGTCGGGCAAACTCCATTGATGAGCGAGCCCTCTTGACAGCTGCGAGGAATTGGGTTAC 5391

Qy 181 AGGAGACAAAGCCGTCAACATATACCTCATCCAGACAGGATCAATCATAGTTAAGCT 240
Db 5392 AGGAGACAAAGCCGTCAACATATACCTCATCCAGACAGGATCAATCATAGTTAAGCT 5451

Qy 241 CCTCCCGAAATCTGCCAAGATAAGGAGGATGTGCCAAGAGCCCTTTGGATGCATACAA 300
Db 5452 CCTCCCGAAATCTGCCAAGATAAGGAGGATGTGCCAAGAGCCCTTTGGATGCATACAA 5511

Qy 301 CAGGACATGACCACTTTGCTCACCCCTTTGGTGACTCTATCCGTAGGATACAAGATC 360
Db 5512 CAGGACATGACCACTTTGCTCACCCCTTTGGTGACTCTATCCGTAGGATACAAGATC 5571

Qy 361 TGTGACTACATCTGGAGGGGGAGACAGGGCGCTTATAGGCGCAATTTATGGCGGTG 420
Db 5572 TGTGACTACATCTGGAGGGGGAGACAGGGCGCTTATAGGCGCAATTTATGGCGGTG 5631

Qy 421 GGCTCTTGGGTTGCAACTGCGGCACAAATAACAGCGCGCGAGCTCTGATACAAGCCAA 480
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Db 5632 GGCTCTTGGGTTGCAACTGCGGCACAAATAACAGCGCGCGAGCTCTGATACAAGCCAA 5691
Qy 481 ACAAATGTCGCCAAACATCTCCGACTTAAAGAGAGCAATTCGCCGCAACCAATGAGCTGT 540
Db 5692 ACAAATGTCGCCAAACATCTCCGACTTAAAGAGAGCAATTCGCCGCAACCAATGAGCTGT 5751
Qy 541 GCATGAGTCACTGACCGGATTATCGCAAATTAGCAGTGGCAGATTGGGAAAGATGACAGATT 600
Db 5752 GCATGAGTCACTGACCGGATTATCGCAAATTAGCAGTGGCAGATTGGGAAAGATGACAGATT 5811
Qy 601 TGTAAATGACCAATTTAATAAACAAGCTCAGGAATTAGACTGCAATCAAAATTGCAACGCA 660
Db 5812 TGTAAATGACCAATTTAATAAACAAGCTCAGGAATTAGACTGCAATCAAAATTGCAACGCA 5871
Qy 661 AGTTGTTAGAGCTCAACCTGTACCTAACCGAATTGACTACAGTATTCGGACCAAAAT 720
Db 5872 AGTTGTTAGAGCTCAACCTGTACCTAACCGAATTGACTACAGTATTCGGACCAAAAT 5931
Qy 721 CACTTCACTGCTTTAAACAAGCTGACTATTACAGGCACTTTACAATCTAGCTGCTGGA 780
Db 5932 CACTTCACTGCTTTAAACAAGCTGACTATTACAGGCACTTTACAATCTAGCTGCTGGA 5991
Qy 781 TATGATTACTTATTACCTAAGTTAGGTGAGGAAACAATCAACTCAGCTCATTAATCGG 840
Db 5992 TATGATTACTTATTACCTAAGTTAGGTGAGGAAACAATCAACTCAGCTCATTAATCGG 6051
Qy 841 TAGCGGCTTAATCACCGGTAAACCTTATTCTATACGACTCACAGCTCAACTCTTGGGTAT 900
Db 6052 TAGCGGCTTAATCACCGGTAAACCTTATTCTATACGACTCACAGCTCAACTCTTGGGTAT 6111
Qy 901 ACAGGTAACTCTACCTTTCAGTCCGGAACTTAAATAATATGCGTGCCCACTTCTGGAAC 960
Db 6112 ACAGGTAACTCTACCTTTCAGTCCGGAACTTAAATAATATGCGTGCCCACTTCTGGAAC 6171
Qy 961 CTTATCCGTAAGCAACCAACAGGGGATTTGCTCGGCACTTGTGCCAAAAGTGGTGACACA 1020
Db 6172 CTTATCCGTAAGCAACCAACAGGGGATTTGCTCGGCACTTGTGCCAAAAGTGGTGACACA 6231
Qy 1021 GGTGGTCTGTGATAGAGAACTTCACACCTCATACTGTATAGAACTGACTTAGATTT 1080
Db 6232 GGTGGTCTGTGATAGAGAACTTCACACCTCATACTGTATAGAACTGACTTAGATTT 6291
Qy 1081 ATATTGTCAAGAATAAGTAAACGTTCCCTATGTCCTGGTATTATTCTCTGCTTGAGCGG 1140
Db 6292 ATATTGTCAAGAATAAGTAAACGTTCCCTATGTCCTGGTATTATTCTCTGCTTGAGCGG 6351
Qy 1141 CAATACGTGGGCTGTATGTACTCAAAAGACCGAAGCGGCACTTATACCAATATGAC 1200
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Qy 1201 TATCAAGGTTGAGTTCATGCCCAACTGCAAGATGACAACTAGATGTGTAAACCCCC 1260
Db 6412 TATCAAGGTTGAGTTCATGCCCAACTGCAAGATGACAACTAGATGTGTAAACCCCC 6471
Qy 1261 GGGTATCATATCGCAAAAATAAGGAGACCGGTGCTCTAAATAGATAAAACAATCATGCAA 1320
Db 6472 GGGTATCATATCGCAAAAATAAGGAGACCGGTGCTCTAAATAGATAAAACAATCATGCAA 6531
Qy 1321 TGTTTATCTTTAGGCGGGATAACTTTAAGGCTCAGTGGGGAATTGATGTAACTTATCA 1380
Db 6532 TGTTTATCTTTAGGCGGGATAACTTTAAGGCTCAGTGGGGAATTGATGTAACTTATCA 6591
Qy 1381 GAAGATATCTCAATACAAGATTTCTCAAGTAATAATAACAGGCAATCTTGATATCTCAAC 1440
Db 6592 GAAGATATCTCAATACAAGATTTCTCAAGTAATAATAACAGGCAATCTTGATATCTCAAC 6651
Qy 1441 TGAGCTTTGGGAATGTCAAACAACCTCGATCAGTAACTGCTTTGAATAAGTTAGGAAAGCAA 1500
Db 6652 TGAGCTTTGGGAATGTCAAACAACCTCGATCAGTAACTGCTTTGAATAAGTTAGGAAAGCAA 6711
Qy 1501 CAGAAAATAGACAAAGTCAATGTCAAACTGACTAGCACTCTGCTCTCAATTCCTATAT 1560
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Db 6712 CAGAAACTAGACAAAGTCAATGTCAAACTGACACGACATCTGCTCTCATTAACCTATAT 6771
Qy 1561 CGTTTTGACTATCATATCTCTGTTTTTGGTATATCTAGCCTGATTCCTAGCAATGCTACCT 1620
Db 6772 CGTTTTGACTATCATATCTCTGTTTTTGGTATATCTAGCCTGATTCCTAGCAATGCTACCT 6831
Qy 1621 AATGTACAGCAAAAGGCGCAACAAAACCTTATATGCTTGGGATATATCTCTAGA 1680
Db 6832 AATGTACAGCAAAAGGCGCAACAAAACCTTATATGCTTGGGATATATCTCTAGA 6891
Qy 1681 TCAGATGAGGCCACTACAAAATGTGAACACAGATGAGGAACGAAGGTTTCCCTAATAG 1740
Db 6892 TCAGATGAGGCCACTACAAAATGTGAACACAGATGAGGAACGAAGGTTTCCCTAATAG 6951
Qy 1741 TAATTTGTGAAAGTTCTGCTAGTCTGTCTAGTTCTAGAGTTAAGAAAAAATACCGGT 1800
Db 6952 TAATTTGTGAAAGTTCTGCTAGTCTGTCTAGTTCTAGAGTTAAGAAAAAATACCGGT 7011
Qy 1801 TGTAGATGACCAAGGACGATATACGGGTAGAAACGTTAAGAGAGCGCCCTCAATTGC 1860
Db 7012 TGTAGATGACCAAGGACGATATACGGGTAGAAACGTTAAGAGAGCGCCCTCAATTGC 7071
Qy 1861 GAGCAGGCTTCACAACTCCGTTCTACCGCTTCACCGACAAACAGTCTCTCAATCATGGAC 1920
Db 7072 GAGCAGGCTTCACAACTCCGTTCTACCGCTTCACCGACAAACAGTCTCTCAATCATGGAC 7131
Qy 1921 CGCCCGTTAGCCAAAGTTGCTTAGAAGATGATGAAGAGAGGCAAAAAATACATGGCGC 1980
Db 7132 CGCCCGTTAGCCAAAGTTGCTTAGAAGATGATGAAGAGAGGCAAAAAATACATGGCGC 7191
Qy 1981 TTGATATCCGGATGCAATCTTATCTTAAACAGTAGACCTTGGCTTATATCTGTAGCC 2040
Db 7192 TTGATATCCGGATGCAATCTTATCTTAAACAGTAGTAGCTTGGCTTATATCTGTAGCC 7251
Qy 2041 TCCCTTTTATATACATGCGGGCTAGCACCTAGCGATCTTGTAGGCATACCGCTAGG 2100
Db 7252 TCCCTTTTATATACATGCGGGCTAGCACCTAGCGATCTTGTAGGCATACCGCTAGG 7311
Qy 2101 ATTTCCAGGCGAGAAAGAAATACATCTACACTTGGTTCCAACTCAAGATGTAGTAGAT 2160
Db 7312 ATTTCCAGGCGAGAAAGAAATACATCTACACTTGGTTCCAACTCAAGATGTAGTAGAT 7371
Qy 2161 AGGATATATAGCAAGTGGCCCTTGAGTCTCCGTTGGCATGTTAAATACGTGAGACACA 2220
Db 7372 AGGATATATAGCAAGTGGCCCTTGAGTCTCCGTTGGCATGTTAAATACGTGAGACACA 7431
Qy 2221 ATTATGACGCAATAACATCTCTCTTATCAGATTAATGGAGCTGCAAAACACAGTGGG 2280
Db 7432 ATTATGACGCAATAACATCTCTCTTATCAGATTAATGGAGCTGCAAAACACAGTGGG 7491
Qy 2281 TGGGGGCGACCTATCCATGACCCAGATTATATAGGGGGGATAGGCAAGAACTCATTTGTA 2340
Db 7492 TGGGGGCGACCTATCCATGACCCAGATTATATAGGGGGGATAGGCAAGAACTCATTTGTA 7551
Qy 2341 GATGATGCTAGTGATGACATCATCTATCCCTCTGCAATTTCAAGAACATCTGAATTTT 2400
Db 7552 GATGATGCTAGTGATGACATCATCTATCCCTCTGCAATTTCAAGAACATCTGAATTTT 7611
Qy 2401 ATCCCGGCGCTACTACAGGATCAGGTTGCACTCGAATACCTCATTTTGACATGAGTCT 2460
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Qy 2461 ACCCATTAAGTCTACACCCATAAGTAAATATGCTGATGACAGATCACTACATTTCA 2520
Db 7672 ACCCATTAAGTCTACACCCATAAGTAAATATGCTGATGACAGATCACTACATTTCA 7731
Qy 2521 TATCAGTATTTAGCATTTGGTGTCTCCGACATCTGCAACAGGAGGATTTCTTTTCT 2580
Db 7732 TATCAGTATTTAGCATTTGGTGTCTCCGACATCTGCAACAGGAGGATTTCTTTTCT 7791
Qy 2581 ACTCTGGTTCCATCAACCTGAGACACACCAAAATCGGAAGTCTTCAGTGTGAGTGCA 2640
Db 7792 ACTCTGGTTCCATCAACCTGAGACACACCAAAATCGGAAGTCTTCAGTGTGAGTGCA 7851

Qy 2641 ACTCCCCCTGGGTTGTGATATGCTGTGCTCGAAAGTCAAGGAGACAGAGGAAGATATAT 2700
Db 7852 ACTCCCCCTGGGTTGTGATATGCTGTGCTCGAAAGTCAAGGAGACAGAGGAAGATATAT 7911
Qy 2701 AACTCAGCTGTCCCTACGCGATGCTATCGGAGGTTAGGTTTCGACGGCCAGTACCAC 2760
Db 7912 AACTCAGCTGTCCCTACGCGATGCTATCGGAGGTTAGGTTTCGACGGCCAGTACCAC 2791
Qy 2761 GAAAAGGACCTAGATGTCAACAATATTTCGGGACCTGGGTGGCCAACTACCCAGGAGTA 2820
Db 7972 GAAAAGGACCTAGATGTCAACAATATTTCGGGACCTGGGTGGCCAACTACCCAGGAGTA 8031
Qy 2821 GGGGGTGGATCTTTTATTGACAGCGCGTATGTTTCTCAGTCTACGGAGGTTTAAACCC 2880
Db 8032 GGGGGTGGATCTTTTATTGACAGCGCGTATGTTTCTCAGTCTACGGAGGTTTAAACCC 8091
Qy 2881 AATTCACCCAGTGCACCTGTACAGGAAGGAAATATGTGATATACAAAGCGATACATGAC 2940
Db 8092 AATTCACCCAGTGCACCTGTACAGGAAGGAAATATGTGATATACAAAGCGATACATGAC 8151
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Db 8212 CGGTTTGGTGGAAAAACATACAGCAGCGCTATCTTATCTATCAAGGTGTCAACATCTCTTA 8271
Qy 3061 GCGGAGACCCGCTACTGCTACCGCCCAACACAGTCACTCATGCGGGCCGGAAGGC 3120
Db 8272 GCGGAGACCCGCTACTGCTACCGCCCAACACAGTCACTCATGCGGGCCGGAAGGC 8331
Qy 3121 AGAATTCCTCAGTAGGAGCATCTCATTCTTGTATCAAGAGGTCTATCATCTTCTCT 3180
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Qy 3181 CCGCGTTATATATCTATCTGACAGTCAAGCAAAAAACAGCCTCTTCATAGTCTTAT 3240
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Qy 3241 ACATTCAGTCCCTCACTCGCCAGGTAGTATCCCTTCCAGGCTTCAGCAAGATGCC 3300
Db 8452 ACATTCAGTCCCTCACTCGCCAGGTAGTATCCCTTCCAGGCTTCAGCAAGATGCC 8511
Qy 3301 AACTCGTGTCTACTGGAGTCTATACAGATCCATATCCCTTAATCTTCTATAGAAACC 3358
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RESULT 8

US-10-440-419-56

; Sequence 56, Application US/10440419

; Publication No. US20030224017A1

; GENERAL INFORMATION:

; APPLICANT: HUANG, ZHUHUI

; APPLICANT: SAMAL, SIBA K.

; TITLE OF INVENTION: RECOMBINANT NEWCASTLE DISEASE VIRUSES USEFUL AS

; FILE OF INVENTION: 108172-00096

; CURRENT APPLICATION NUMBER: US/10/440,419

; PRIOR FILING DATE: 2003-05-19

; PRIOR FILING DATE: 2003-05-19

; PRIOR FILING DATE: 2002-03-06

; PRIOR FILING DATE: 2000-05-05

; PRIOR FILING DATE: 2002-05-17

; PRIOR FILING DATE: 1999-12-16

; PRIOR FILING DATE: 1999-05-05

; NUMBER OF SEQ ID NOS: 56

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 56

; LENGTH: 15882

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Recombinant cDNA for NDV

US-10-440-419-56

Query Match 95.28; Score 3198; DB 17; Length 15882;
Best Local Similarity 97.08; Pred. No. 0;
Matches 3258; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

QY 1 ACGGTAGAGATTCTCGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGCTCCAGACC 60
DB 4498 ACGGTAGAGATTCTCGATCCCGGTTGGCGCCCTCTAGGTGCAGNATGGGCCCCAGACC 4557

QY 61 TTCTACCAAGAACCCAGCACTATGATGTGACTATCCGGGTTGCGCTGGCACTGAGTTG 120
DB 4558 TTCTACCAAGAACCCAGTACTATGATGTGACTGTCCGAGTCCGCTGCTACTGAGTTG 4617

QY 121 CATCTGTCGGCAAACTCCATTGATGTCAGCGCCCTCTTGCACTGTCAGGAATTGTGGTTAC 180
DB 4618 CATCTGTCGGCAAACTCCATTGATGTCAGCGCCCTCTTGCGGCTGTCAGGAATTGTGGTTAC 4677

QY 181 AGGAGACAAAGCCGTCAACATATACCTCATCCAGACAGGATCAATCATAGTTAAGCT 240
DB 4678 AGGAGACAAAGCAGTCAACATATACCTCATCCAGACAGGATCAATCATAGTTAAGCT 4737

QY 241 CCTCCGGAATCTGCCAAGGATAGGAGGATGTGCGAAAGCCCCCTTGGATGCATACAA 300
DB 4738 CCTCCGGAATCTGCCAAGGATAGGAGGATGTGCGAAAGCCCCCTTGGATGCATACAA 4797

QY 301 CAGGACATTGACACATTGCTCACCCTTGTGTGACTCTATCCGTAGGATACAGAGTC 360
DB 4798 CAGGACATTGACACATTGCTCACCCTTGTGTGACTCTATCCGTAGGATACAGAGTC 4857

QY 361 TGTGACTACATCTGGAGGGGGAGACAGGGCGCTTATAGGCGCCATTATTCGGCGTGT 420
DB 4858 TGTAACTACATCTGGAGGGGGAGACAGAAACGCTTATAGGCGCCATTATTCGGCGTGT 4917

QY 421 GGCTCTGGGGTTGCAACTCCCGCACAAATTAACAGCGCCCGCAGCTCTGTATACAAGCCAA 480
DB 4918 GGCTCTGGGGTTGCAACTCTGCACAAATAACAGCGCCCGCAGCTCTGTATACAAGCCAA 4977

QY 481 ACAAAATGCTGCCAATCTCCGACTTAAAGAGAGCAATTCGCCCAACCAATGAGGCTGT 540
DB 4978 ACAAAATGCTGCCAATCTCCGACTTAAAGAGAGCAATTCGCCCAACCAATGAGGCGGT 5037

QY 541 GCATGAGTCACTGACGGATTATCGCAACTAGCAGTGGCAGTTTGGGAAGATGACGAGTT 600
DB 5038 GCATGAGTCACTGACGGATTATCGCAACTAGCAGTGGCAGTTTGGGAAGATGACGAGTT 5097

QY 601 TGTAAATGACCAATTTAATAAAACAGCTCAGGAATTAGACTGCATCAAAATTCGACAGCA 660
DB 5098 TGTAAATGACCAATTTAATAAAACAGCTCAGGAATTAGACTGCATCAGAAATTCGACAGCA 5157

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DB 5158 AGTTGGTGTAGAGCTCAACCTGTACCTAACCGAATTGACTACAGTATTCGGACCAAAAT 5217

QY 721 CACTTCACCTGCTTTAAACAAGCTGACTATTTCAGGCACCTTTACAATCTAGCTCGTGAAA 780
DB 5218 CACTTCACCTGCTTTAAACAAGCTGACTATTTCAGGCACCTTTACAATCTAGCTCGTGAAA 5277

QY 781 TATGGATTACTTATGACTAAGTTAGGTGTAGGGAACAATCAACTCAGCTCATTAATCGG 840
DB 5278 TATGGATTACTTATGACTAAGTTAGGTGTAGGGAACAATCAACTCAGCTCATTAATCGG 5337

QY 841 TAGCGGCTTAATCAGCGGTAACCTTATCTATACGACTACAGACTCAACTCTTGGGTAT 900
DB 5338 TAGCGGCTTAATCAGCGGTAACCTTATCTATACGACTACAGACTCAACTCTTGGGTAT 5397

QY 901 ACAGGTAACTCTACCTTCAGTCGGGAACCTAAATAATATATCGTCGCACCTACTTGGAAAC 960
DB 5398 ACAGGTAACTCTACCTTCAGTCGGGAACCTAAATAATATATCGTCGCACCTACTTGGAAAC 5457

QY 961 CTTATCCGTAAGCACAAACCGGGGATTTGCCTCGGCACCTTGTCCAAAAGTGTGTGACACA 1020
DB 5458 CTTATCCGTAAGCACAAACCGGGGATTTGCCTCGGCACCTTGTCCAAAAGTGTGTGACACA 5517

QY 1021 GGTCCGGTCTGTGATAGAGAACTTCACACCTCATCTGATATAGAAACTGACTTACATTTT 1080
DB 5518 GGTCCGGTCTGTGATAGAGAACTTCACACCTCATATGTATAGAAACCGACCTTGGATTT 5577

QY 1081 ATATTCTACAAGAAATAGTAACGTTCCCTATGTCCCTCGTGTATTTATTCCTGCTTGAGCGG 1140
DB 5578 ATATTCTACAAGAAATAGTAACATTCCTATGTCCCTCGTGTATTTATTCCTGCTTGAGCGG 5637

QY 1141 CAATACGTCCGCTGTATGTACTCAAAAGACCGAAGGCGACTTACTACACATACATGAC 1200
DB 5638 CAATACATCCGCTGTATGTACTCAAAAGACCGAAGGCGCACTCACTACGCCATACATGAC 5697

QY 1201 TATCAAGGTTTCAGTTCATCGCCAACTGCAAGATGACAACATGTAGATGTGTAAACCCCC 1260
DB 5698 TATCAAGGTTTCAGTTCATCGCTAACTGCAAGATGACAACATGTAGATGTGTAAACCCCC 5757

QY 1261 GGGTATCATATCGCAAAACTATGGAAGCCGCTGTCTCTAATAGATAAAACAATCATGCAA 1320
DB 5758 GGGTATCATATCGCAAAACTATGGAAGCCGCTGTCTCTAATAGATAAGCAATCATGCAA 5817

QY 1321 TGTATTATCCTTAGGCGGGATACCTTTAAGGCTCAGTGGGGAATTCGATGTAACTTATCA 1380
DB 5818 TGTATTATCCTTAGAGCGGGATACCTTTAAGGCTCAGTGGGGAATTCGATGTAACTTATCA 5877

QY 1381 GAAGAAATCTCAATCAAGATTTCTCAAGTAAATAAAGAGCAATCTTGATATCTCAAC 1440
DB 5878 GAAGAAATCTCAATCAAGATTTCTCAAGTAAATAAAGAGCAATCTTGATATCTCAAC 5937

QY 1441 TGAGCTTGGGAATGTCAACAACTCGATCAGTAACTGCTTTGAAATAAGTTAGAGGAAGCAA 1500
DB 5938 TGAGCTTGGGAATGTCAACAACTCGATCAGTAACTGCTTTGAAATAAGTTAGAGGAAGCAA 5997

QY 1501 CAGAAATAGACAAAGTCAATGTCAAACTGACTAGACATCTGTCTCTCATTAACCTATAT 1560
DB 5998 CAGAAATAGACAAAGTCAATGTCAAACTGACTAGACATCTGTCTCTCATTAACCTATAT 6057

QY 1561 CGTTTGTGACTATCATATCTCTTGTGTTTGGTATACCTAGCTGATCTAGCATGCTACCT 1620
DB 6058 CGTTTGTGACTATCATATCTCTTGTGTTTGGTATACCTAGCTGATCTAGCATGCTACCT 6117

QY 1621 AATGTACAAAGCAAAAGCGCAACAAAAAACCTTATTATGGCTTGGGAATAATACTCTAGA 1680
DB 6118 AATGTATAGCAAAAGCGCAACAAAAAGACCTTATTATGGCTTGGGAATAATACTCTAGA 6177

QY 1681 TCAGATGAGAGCCACTACAAAAATGTGAACACAGATGAGGAACGAAGTTTCCCTAATAG 1740
DB 6178 TCAGATGAGAGCCACTACAAAAATGTGAACACAGATGAGGAACGAAGTTTCCCTAATAG 6237

QY 1741 TAATTTGTGTGAAAAGTTCTGGTAGTCTGTCTGAGTTTACAGAGTTTAAAGAAAACTACCGGT 1800
DB 6238 TAATTTGTGTGAAAAGTTCTGGTAGTCTGTCTGAGTTTACAGAGTTTAAAGAAAACTACCGGT 6297

QY 1801 TGTAGATGACCAAGGACGATATACGGGTAGAAACGGTAAAGAGGCGCGCCCTCAATTGC 1860
DB 6298 TGTAGATGACCAAGGACGATATACGGGTAGAAACGGTAAAGAGGCGCGCCCTCAATTGC 6357

QY 1861 GAGCCAGGCTTCAACCTCCGTTCTACCGCTTACCGCAACAACAGTCTCTCAATCATGGAC 1920
DB 6358 GAGCCAGGCTTCAACCTCCGTTCTACCGCTTACCGCAACAACAGTCTCTCAATCATGGAC 6417

QY 1921 CGGCGCTTAGCCCAAGTTGGTTAGAGAAATGATGAAGAGGAGCAAAATATACATGCGGC 1980
DB 6418 CGGCGCTTAGCCCAAGTTGGTTAGAGAAATGATGAAGAGGAGCAAAATATACATGCGGC 6477

QY 1981 TTGATATTCCGGATTGCAATCTTTATTCTTAAACAGTAGTAGCTTGGCTATATCTGTAGCC 2040

Db 6478 TGGATATTCGGGATTGCAATCTTACTCTTAACAGTAGTGACCTTAGCTACATCTGTAGCC 6537
Qy 2041 TCCCTTTTATATAGCATGGGGCTAGCACACCTAGCGATCTTTGTAGGCATACCCGACTAGG 2100
Db 6538 TCCCTTGTATATAGCATGGGGCTAGCACACCTAGCGACCTTGTAGGCATACCCGACGAG 6597
Qy 2101 ATTTCCAGGCGAGAAAGAAATTAATCATCTACACTTTGGTTCCAAATCAAGATGTAGTAGAT 2160
Db 6598 ATTTCTAGGCGAGAAAGAAATTAATCATCTGCACTTGGTTCCAAATCAAGATGTAGTAGAT 6657
Qy 2161 AGGATATATAGCAAGTGGCCCTTGAGTCTCGTTGGCATTTGTTAAATCATCTGAGACACACA 2220
Db 6658 AGGATATATAGCAAGTGGCCCTTGAGTCTCGTTGGCATTTGTTAAACACTGAGACACACA 6717
Qy 2221 ATATGAACGCAATAACATCTCTCTCTTATCAGATTAATGGAGCTGCAAAACAAAGTGGG 2280
Db 6718 ATATGAACGCAATAACATCTCTCTCTTATCAGATTAATGGAGCTGCGAAACAAAGCGGG 6777
Qy 2281 TGGGGGGCACTATCCATGACCCAGATTAATATAGGGGGGATAGGCAAAAGAACTCAATTGTA 2340
Db 6778 TGGGGGGCACTATCCATGACCCAGATTTTATCGGGGGGATAGGCAAAAGAACTCAATTGTA 6837
Qy 2341 GATGATGCTAGTGTGCATCATCTCTATCCCTCTGCATTTCAAGACATCTGAATTTT 2400
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Qy 2401 ATCCCGGCGCTACTACAGGATCAGGTTGCACTCGAATACCCCTCATTTGACATGAGTGCT 2460
Db 6898 ATCCCGGCGCTACTACAGGATCAGGTTGCACTCGGATACCTCATTTGACATGAGTGCT 6957
Qy 2461 ACCCATTAAGTACACCCATAATGTAATGTTGCTGGAAGTACAGAGATCACTCAATTCAC 2520
Db 6958 ACCCATTAAGTACACCTATAATGTAATGTTGCTGGAAGTACAGAGATCACTCAACTCA 7017
Qy 2521 TATCAGTATTTAGCATTTGGTGTCTCCGGACATCTGCAACAGGAGGATTTCTTTTCT 2580
Db 7018 CATCAGTATTTAGCATTTGGTGTCTCCGGACAACTGCAACAGGAGGATTTCTTTTCT 7077
Qy 2581 ACTTCGGTTCATCAACCTCGACACACCCAAATCGGAAGTCTTGCAAGTGTAGTGCA 2640
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Qy 2641 ACTCCCTGGGTTGTATGATCTGTGCTCGAAAGTACGGAGACAGAGAAAGAAATPAT 2700
Db 7138 ACTCCCTTAGGTTGTGATGATGCTGTGCTCGAAAGTACGGAGACAGAGAAAGAAATPAT 7197
Qy 2701 AACTCAGCTGTCCCTACCGGATGATGATGGAGGTTAGGTTTCGACGGCCAGTACCAC 2760
Db 7198 AACTCAGCTGTCCCTACCGATGATGATGGAGGTTAGGTTTCGACGGCCAAATACCAC 7257
Qy 2761 GAAAGGACCTAGATGTCACAACTATTTTCGGGACTGGGTGGCCAACTACCCAGGAGTA 2820
Db 7258 GAAAGGACCTAGATGTCACAACTATTTTCAGGACTGGGTGGCCAACTACCCAGGAGTA 7317
Qy 2821 GGGGGTGGATCTTTTATTGACAGCGCGGTATGGTTCTCAGTCTACGGAGGGTTAAACCC 2880
Db 7318 GGGGGTGGATCTTTTATTGACAGCGCGGTATGGTTCTCAGTCTACGGAGGGTGAACCC 7377
Qy 2881 AATTCAACCACTGACACTGTACAGGAGGAAATATGTGATATACAGCGATCAATGAC 2940
Db 7378 AATTCAACCACTGACACTGTACAGGAGGAAATATGTGATATACAGCGATCAATGAC 7437
Qy 2941 ACATGCCAGATGAGCAAGACTTACCAGATTCGAATGGCCAAAGTCTTCGTATTAAGCCTGGA 3000
Db 7438 ACATGCCAGATGAGCAAGACTTACCAGATTCGAATGGCCAAAGTCTTCGTATTAAGCCTGGA 7497
Qy 3001 CGGTTTGGTGGGAAACGATACAGCAGGCTATCTTATCTATCAAGGTTGCAACATCTTTA 3060
Db 7498 CGGTTTGGTGGGAAACGATACAGCAGGCTATCTTATCTATCAAGGTTGCAACATCTTTG 7557
Qy 3061 GGGCAAGACCCGGTATCTGATACCGCCCAACACAGTCACTCATGGGGGGCGAAGGC 3120

Db 7558 GGGCAAGACCCAGTACTGACTGTACCGCCCAACACAGTCACTCATGGGGGGCGAAGGC 7617
Qy 3121 AGAATTTCTCAGTAGGGACATCTCAATTTCTGTATCAACGAGGCTCATCATCTTCTCT 3180
Db 7618 AGAATTTCTCAGTAGGGACATCTCAATTTCTGTATCAGCGAGGCTCATCATCTTCTCT 7677
Qy 3181 CCGGGTTATTATATCTCTATCAGTCAAGCAACAAAGAGCCACTCTTCATAGTCCCTAT 3240
Db 7678 CCGGGTTATTATATCTCTATCAGTCAAGCAACAAAGAGCCACTCTTCATAGTCCCTAT 7737
Qy 3241 ACATTTCAATGCTTCACTCGGCCAGGTAGTATCCCTTCCAGGCTTCAGCAAGATGCCCC 3300
Db 7738 ACATTTCAATGCTTCACTCGGCCAGGTAGTATCCCTTCCAGGCTTCAGCAAGATGCCCC 7797
Qy 3301 AACTCGTGTGTACTGGAGTCTATACAGATCCATATCCCTTAATCTTCTATAGAAACC 3358
Db 7798 AACTCGTGTGTACTGGAGTCTATACAGATCCATATCCCTTAATCTTCTATAGAAACC 7855

RESULT 9
US-09-881-457A-1
; Sequence 1, Application US/09881457A
; Patent No. US20020081316A1
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D
; APPLICANT: Cook, Stephanie M
; APPLICANT: Wild, Martha A
; TITLE OF INVENTION: No. US20020081316A1el Avian Herpes Virus and Uses Thereof
; FILE REFERENCE: SY01105K1QKOK
; CURRENT APPLICATION NUMBER: US/09/881,457A
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 09/426,352
; PRIOR FILING DATE: 1999-10-25
; PRIOR APPLICATION NUMBER: 08/804,372
; PRIOR FILING DATE: 1997-02-21
; PRIOR APPLICATION NUMBER: PCT/US95/10245
; PRIOR FILING DATE: 1995-08-09
; PRIOR APPLICATION NUMBER: 08/663,566
; PRIOR FILING DATE: 1996-06-13
; PRIOR APPLICATION NUMBER: 08/288,065
; PRIOR FILING DATE: 1994-08-09
; PRIOR APPLICATION NUMBER: PCT/US93/05681
; PRIOR FILING DATE: 1993-06-14
; PRIOR APPLICATION NUMBER: 08/023,610
; PRIOR FILING DATE: 1993-02-26
; PRIOR APPLICATION NUMBER: 07/898,087
; PRIOR FILING DATE: 1992-06-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3570
; TYPE: DNA
; ORGANISM: Newcastle disease virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1194)..(2888)
; OTHER INFORMATION: NDV Fusion Protein
; NAME/KEY: misc feature
; LOCATION: (1355)
; OTHER INFORMATION: n = any nucleotide
; US-09-881-457A-1

Query Match 50.7%; Score 1701.6; DB 9; Length 3570;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 1749; Conservative 0; Mismatches 25; Indels 3; Gaps 3;
Qy 16 TGGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACCTTCTTACCAAGAACCC 75
Db 1199 TCGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACCTTCTTACCAAGAACCC 1258
Qy 76 AGCACTTATGATGCTGACTATCCGGTTGCCCTGGCACTGAGTTGCATCTGTCCGGCAAA 135
Db 1259 AGCACTTATGATGCTGACTATCCGGTTGCCCTGGCACTGAGTTGCATCTGTCCGGCAAA 1318

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136 CTCAATTGATGGAGGCTCTTGAGCTGAGGAATTTGGTTACAGGAGACAAAGCCGT 195
1319 CTCCATTGATGGAGGCTCTTGAGCTGAGG-ACNTGGTTACAGGAGCAAGCAAT 1377
196 CAACATATACCTCACTCCAGACAGGATCAATCATATAGTTAAGTCTCCCGAATCTGCC 255
1378 CAACATATACACCTCACTCCAGACAGG-TCAATCATAT-TTAAGTCTCCCGAATCTGCC 1435
256 CAAGGATAAGAGGATGTCGGAAGCCCTTGGATGCATACACAGGACATTTGACCAC 315
1436 AAAGGATAAGAGGATGTCGGAAGCCCTTGGATGCATACACAGGACATTTGACCAC 1495
316 TTTGCTCAACCCCTTGGTCACTCTATCCGTAGGATCAAGAGTCTGTGACTACATCTGG 375
1496 TTTGCTCAACCCCTTGGTCACTCTATCCGTAGGATCAAGAGTCTGTGACTACATCTGG 1555
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1556 AGGGGGAGACAGGGGCGCTTATAGCGGCATTTATTTGGCGGTGTGGCTCTTGGGGTGC 1615
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1616 AACTGCGGCAAAATTAACAGCGCGCAGCTCTGTATCAAGCCAAACAAAATGTCGCAA 1675
496 CATCTCTCGACTTAAAGAGAGCATTTGCCGCAACCAATGAGGCTGTGATGAGGTCACTGA 555
1676 CATCTCTCGACTTAAAGAGAGCATTTGCCGCAACCAATGAGGCTGTGATGAGGTCACTGA 1735
556 CGGATTATCGCAACTAGCAGTGGCAGTTGGGAAGATGACAGTGTGTTTAAATGACCAATT 615
1736 CGGATTATCGCAACTAGCAGTGGCAGTTGGGAAGATGACAGTGTGTTTAAATGACCAATT 1795
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1796 TAATAAAAGCTCAGGAATTAGACTGCATCAAAATTTGCACAGCAAGTTGGTTAGAGCT 1855
676 CAACCTGTACTTAACCGAATTTGACTACAGTATTTGGGACCAAAATCACTTCACTGCTTT 735
1856 CAACCTGTACTTAACCGAATTTGACTACAGTATTTGGGACCAAAATCACTTCACTGCTTT 1915
736 AAACAAGCTGACTATTTCAGGCACCTTTTACAACTAGCTGGTGGAAATATGGATTACTTAT 795
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796 GACTAAGTTAGTGTAGGGAACCAATCAACTCAGCTTCAATTCGGTAGCGGCTTAATCAC 855
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856 CGGTAACCCCTATTCTATACGACTCACAGACTCAACTCTTGGGTATACAGGTAACTCTACC 915
2036 CGGTAACCCCTATTCTATACGACTCACAGACTCAACTCTTGGGTATACAGGTAACTCTACC 2095
916 TTCAGTGGGAACCTAAATATATGCTGCGCACCTACTTTGGAAACCTTATCCGTAAGCAC 975
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976 AACAGGGGATTTGCTCGGCACTTGTGCCAAAAGTGGTGAACAGTCCGTTCTGTGAT 1035
2156 AACAGGGGATTTGCTCGGCACTTGTGCCAAAAGTGGTGAACAGTCCGTTCTGTGAT 2215
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2216 AGAAGAACTTGACACCTCATCTGTATAGAACTGACTTAGATTATATTGTACAAGAAAT 2275
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1216 CATCGCAACTGCAAGATGACAAATGATAGATGTAAACCCCGGGTATCATATCGCA 1275
2396 CATCGCTAACTGCAAGATGACAAATGATAGATGTAAACCCCGGGTATCATATCGCA 2455
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2456 AAATATGAGGAAGCCGTGCTCTTAATAGATAAACAATCATGCAATGTTTATCTCTAGG 2515
1336 CGGGATAAATTTAAGGCTCAGTGGGAATTTGATGTAACCTTATCAGAAGAAATCTCAAT 1395
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1396 ACAAGATTCTCAAGTAAATAAACAAGCAATCTTGTATATCTCAACTGAGCTTGGGAATGT 1455
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1456 CAACAACCTCGATCAGTAATGCTTTGTAATTAAGTTAGAGGAAGCAACAGAAAACTAGACAA 1515
2636 CAACAACCTCGATCAGTAATGCTTTGTAATTAAGTTAGAGGAAGCAACAGAAAACTAGACAA 2695
1516 AGTCAATGTCAAACTGACTAGCACATCTGCTCTCATTTACCTATATCGTTTGTACTATCAT 1575
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1636 GGCGCAACAAAAACCTTATTTATGGCTTGGGAATATATCTAGATCAGATGAGAGCCAC 1695
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1696 TACAAAAATGTGAACACAGATGAGGAAGCAAGGTTTCCCTTAATAGTAATTTGTGTGAAG 1755
2876 TACAAAAATGTGAACACAGATGAGGAAGCAAGGTTTCCCTTAATAGTAATTTGTGTGAAG 2935
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2936 TTCTGCTAGTCTCTCAGTTTCAGAGAGTTTAAAGAAAAAA 2972
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RESULT 10

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US-11-126-465-1
; Sequence 1, Application US/11126465
; Publication No. US20050202045A1
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D
; APPLICANT: Cook, Stephanie M
; APPLICANT: Wild, Martha A
; TITLE OF INVENTION: Novel Avian Herpes Virus and Uses Thereof
; FILE REFERENCE: SY01105K1OK
; CURRENT APPLICATION NUMBER: US/11/126,465
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US/09/881,457
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 09/426,352
; PRIOR FILING DATE: 1999-10-25
; PRIOR APPLICATION NUMBER: 08/804,372
; PRIOR FILING DATE: 1997-02-21
; PRIOR APPLICATION NUMBER: PCT/US95/10245
; PRIOR FILING DATE: 1995-08-09
; PRIOR APPLICATION NUMBER: 08/663,566
; PRIOR FILING DATE: 1996-06-13
; PRIOR APPLICATION NUMBER: 08/288,065
; PRIOR FILING DATE: 1994-08-09
; PRIOR APPLICATION NUMBER: PCT/US93/05681
; PRIOR FILING DATE: 1993-06-14
; PRIOR APPLICATION NUMBER: 08/023,610
; PRIOR FILING DATE: 1993-02-26
; PRIOR APPLICATION NUMBER: 07/898,087
; PRIOR FILING DATE: 1992-06-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 1									
; LENGTH: 3570									
; TYPE: DNA									
; ORGANISM: Newcastle disease virus									
; FEATURE:									
; NAME/KEY: CDS									
; LOCATION: (1194)..(2888)									
; OTHER INFORMATION: NDV Fusion Protein									
; FEATURE:									
; NAME/KEY: misc feature									
; LOCATION: (1355)									
; OTHER INFORMATION: n = any nucleotide									
US-11-126-465-1									
Query Match 50.7%; Score 1701.6; DB 24; Length 3570;									
Best Local Similarity 98.4%; Pred. No. 0;									
Matches 1749; Conservative 0; Mismatches 25; Indels 3; Gaps 3;									
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Qy	76	AGCACTATGATGCTGACTATCCGGGTTGCGCTGGCACTGAGTTGCATCTGTCCGGCAAA	135						
Db	1259	AGCACTATGATGCTGACTATCCGGGTTGCGCTGGCACTGAGTTGCATCTGTCCGGCAAA	1318						
Qy	136	CTCCATTGATGGCAGGCTCTTTCAGCTGCGAGGAATTGTGTTACAGGAGACAAAGCCGT	195						
Db	1319	CTCCATTGATGGCAGGCTCTTTCAGCTGCGAGGAATTGTGTTACAGGAGACAAAGCAAT	1377						
Qy	196	CAACATATACACTCATCCGACAGGATCAATCATAGTTAAGTCTCTCCGGAATCTGCC	255						
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Qy	256	CAAGGATAAGGAGGATGTGGGAAGCCCTTGGATGCATACACAGGACATTGACCCAC	315						
Db	1436	ANAGGTAAGGAGGATGTGGGAAGCCCTTGGATGCATACACAGGACATTGACCCAC	1495						
Qy	316	TTTGCTACCCCCCTTGTGACTCTATCCGTAGGATACAGAGTCTGTGACTACATCTGG	375						
Db	1496	TTTGCTACCCCCCTTGTGACTCTATCCGTAGGATACAGAGTCTGTGACTACATCTGG	1555						
Qy	376	AGGGGGGAGACAGGGGCCCTTATAGGCGCCATTATTGGCGGTGTGGCTCTTGGGGTTC	435						
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Qy	496	CATCTCCGACTTAAAGAGAGCATTTGCCCAACCAATGAGGCTGTGCATGAGGTCACTGA	555						
Db	1676	CATCTCCGACTTAAAGAGAGCATTTGCCCAACCAATGAGGCTGTGCATGAGGTCACTGA	1735						
Qy	556	CGGATATCGCAACTAGCAGTGGGAGATGCGAGGATGCGAGTTGTTAATGACCAATT	615						
Db	1736	CGGATATCGCAACTAGCAGTGGGAGATGCGAGGATGCGAGTTGTTAATGACCAATT	1795						
Qy	616	TAATAAAGACGCTCAGGAATTAGACTGCATCAAAATTCGACAGCAAGTTGGTGTAGACT	675						
Db	1796	TAATAAAGACGCTCAGGAATTAGACTGCATCAAAATTCGACAGCAAGTTGGTGTAGACT	1855						
Qy	676	CAACTGTACCTAACCGAATTGACTACAGTATTCCGACCAAAATCACTTCACCTGCTTTT	735						
Db	1856	CAACTGTACCTAACCGAATTGACTACAGTATTCCGACCAAAATCACTTCACCTGCTTT	1915						
Qy	736	AAAAGAGTACTATTACGACCTTTACAACTTCTAGCTGGTGGAAATATGGAATTACTTAT	795						
Db	1916	AAAAGAGTACTATTACGACCTTTACAACTTCTAGCTGGTGGAAATATGGAATTACTTAT	1975						
Qy	796	GACTAAGTACTGTAGGGAACAATCAACTCAGCTCATTAATCGGTAGCGCTTAATCAC	855						
Db	1976	GACTAAGTACTGTAGGGAACAATCAACTCAGCTCATTAATCGGTAGCGCTTAATCAC	2035						

RESULT 11

US-10-838-834-19
; Sequence 19, Application US/10838834
; Publication No. US20050048074A1
; GENERAL INFORMATION:
; APPLICANT: Cardineau, et al.
; TITLE OF INVENTION: Vectors and Cells for Preparing Immunoprotective Compositions

Qy	856	CGGTAAACCCCTATTTCTATACGACTCACAGCTCAACTCTTGGGTATACAGGTAACCTCTACC	915
Db	2036	CGGTAAACCCCTATTTCTATACGACTCACAGCTCAACTCTTGGGTATACAGGTAACCTCTACC	2095
Qy	916	TTCACTCGGGAACCTTAAATAATATATCGTGCCACCTTACCTTGGAAACCTTTATCGTAAGCAC	975
Db	2096	TTCACTCGGGAACCTTAAATAATATATCGTGCCACCTTACCTTGGAAACCTTTATCGTAAGCAC	2155
Qy	976	AACCAAGGGAATTTGCTCGGCACTTGTCCCAAAAGTGTGACACAGGTCGGTCTGTGTAT	1035
Db	2156	AACCAAGGGAATTTGCTCGGCACTTGTCCCAAAAGTGTGACACAGGTCGGTCTGTGTAT	2215
Qy	1036	AGAAGAACTTGACACCTCATATCTGTATAGAAACCTGACTTATATTTATGTACAAAGAT	1095
Db	2216	AGAAGAACTTGACACCTCATATCTGTATAGAAACCTGACTTATATTTATGTACAAAGAT	2275
Qy	1096	AGTAACGTTCCCTATGTCCTGCTGTTATTTATCTCTGCTTGGCGGCAATACGTCGGCCTG	1155
Db	2276	AGTAACGTTCCCTATGTCCTGCTGTTATTTATCTCTGCTTGGCGGCAATACGTCGGCCTG	2335
Qy	1156	TATGTACTCAAGAGCCGACCTTACTACACATATACATGACTATCAAAAGTTTCACT	1215
Db	2336	TATGTACTCAAGAGCCGACCTTACTACACATATATGACTATCAAAAGTTTCACT	2395
Qy	1216	CATCCCAACTGCAAGATGACAAATGATGTGTAAACCCCGGCTATCATATGCA	1275
Db	2396	CATCCCAACTGCAAGATGACAAATGATGTGTAAACCCCGGCTATCATATGCA	2455
Qy	1276	AACTATGGAAGCCGCTGCTCTTAATAGATAAACAATCATGCAATGTTTATCCCTAGG	1335
Db	2456	AACTATGGAAGCCGCTGCTCTTAATAGATAAACAATCATGCAATGTTTATCCCTAGG	2515
Qy	1336	CGGATAACTTTAAGGCTCAGTGGGGAATTCGATGTAACTTATCAGAAGAAATATCTCAAT	1395
Db	2516	CGGATAACTTTAAGGCTCAGTGGGGAATTCGATGTAACTTATCAGAAGAAATATCTCAAT	2575
Qy	1396	ACAAGATTTCAAGTAATAATAACAGGCAATCTTGATATCTCAACTGAGCTTGGGAATGT	1455
Db	2576	ACAAGATTTCAAGTAATAATAACAGGCAATCTTGATATCTCAACTGAGCTTGGGAATGT	2635
Qy	1456	CAACAACCTGATAGTAATGCTTTGAATAAGTTAGAGAAAGCAACAGAACTAGACAA	1515
Db	2636	CAACAACCTGATAGTAATGCTTTGAATAAGTTAGAGAAAGCAACAGAACTAGACAA	2695
Qy	1516	AGTCAATGCTCAAACTGACTAGCACATCTGCTCTCATTAACCTATATCGTTTGGACTATCAT	1575
Db	2696	AGTCAATGCTCAAACTGACTAGCACATCTGCTCTCATTAACCTATATCGTTTGGACTATCAT	2755
Qy	1576	ATCTCTTGTGTTTGGTATACCTTAGCCTGATTTAGCATGCTACCTTAATGTACAAGCAAAA	1635
Db	2756	ATCTCTTGTGTTTGGTATACCTTAGCCTGATTTAGCATGCTACCTTAATGTACAAGCAAAA	2815
Qy	1636	GGCGCAACAAAACCTTATTTATGCTTGGGAATAATCTCTAGATCAGATGAGAGCCAC	1695
Db	2816	GGCGCAACAAAACCTTATTTATGCTTGGGAATAATCTCTAGATCAGATGAGAGCCAC	2875
Qy	1696	TACAAAATGTGAACACAGATGAGAAACGAGGTTTCCCTAATAGTAATTTGTGTGAAG	1755
Db	2876	TACAAAATGTGAACACAGATGAGAAACGAGGTTTCCCTAATAGTAATTTGTGTGAAG	2935
Qy	1756	TTCTGGTAGTCTGTGCTCAGTTCAGAGAGTTTAAAGAAAAA	1792
Db	2936	TTCTGGTAGTCTGTGCTCAGTTCAGAGAGTTTAAAGAAAAA	2972

; TITLE OF INVENTION: Derived from Transgenic Plants
; FILE REFERENCE: 3121/2022
; CURRENT APPLICATION NUMBER: US/10/838,834
; CURRENT FILING DATE: 2004-05-04
; PRIOR APPLICATION NUMBER: US 60/467,998
; PRIOR FILING DATE: 2003-05-05
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 1734
; TYPE: DNA
; ORGANISM: Newcastle disease virus
; US-10-838-834-19

Query Match 42.7%; Score 1434.4; DB 21; Length 1734;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1438; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy	1915	ATGACCGCGCGCTTAGCCAAAGTTGCGTTAGAGAAATGATGAAGAGAGGCGCAAAAATACA	1974
Db	1	ATGACCGCGCGCTTAGCCAAAGTTGCGTTAGAGAAATGATGAAGAGAGGCGCAAAAATACA	60
Qy	1975	TGGCGCTTGATATTCGGGATTCGAAATCTTATTTCTTAAACAGTAGTGA	2034
Db	61	TGGCGCTTGATATTCGGGATTCGAAATCTTATTTCTTAAACAGTAGTGA	120
Qy	2035	GTAGCCCTCCCTTTATATAGCATGGGGCTAGCACCTAGCGATCTTTGAGGCATACCG	2094
Db	121	GTAGCCCTCCCTTTATATAGCATGGGGCTAGCACCTAGCGATCTTTGAGGCATACCG	180
Qy	2095	ACTAGGATTTCCAGGCGAGAGAAAGATTACATCTACACTTGGTTCCAAATCAAGATGTA	2154
Db	181	ACTAGGATTTCCAGGCGAGAGAAAGATTACATCTACACTTGGTTCCAAATCAAGATGTA	240
Qy	2155	GTAGATAGGATATATAAGCAAGTGGCCCTCGAGTCTCGTTGGCAATGTTAAATACAG	2214
Db	241	GTAGATAGGATATATAAGCAAGTGGCCCTCGAGTCTCGTTGGCAATGTTAAATACAG	300
Qy	2215	ACCAATATTGACGCAATTAACATCTCTCTCTTATCAGATTAATGGAGTGCAGAAACAC	2274
Db	301	ACCAATATTGACGCAATTAACATCTCTCTCTTATCAGATTAATGGAGTGCAGAAACAC	360
Qy	2275	AGTGGGTGGGGGCGACCTATCCATGACCCAGATTATATAGGGGGGATAGCCAAAGAACTC	2334
Db	361	AGCGGTGGGGGCGACCTATCCATGACCCAGATTATATAGGGGGGATAGCCAAAGAACTC	420
Qy	2335	ATTGTAGATGATGTAGTGTGACATCATCTATCCCTCTGCAATTTCAAGAAACATCTG	2394
Db	421	ATTGTAGATGATGTAGTGTGACATCATCTATCCCTCTGCAATTTCAAGAAACATCTG	480
Qy	2395	AAATTTATCCCGCGCCTTACTACAGGATCAGGTTGCACTCGAATACCTCATTTGACATG	2454
Db	481	AAATTTATCCCGCGCCTTACTACAGGATCAGGTTGCACTCGAATACCTCATTTGACATG	540
Qy	2455	AGTGCTACCCATTTACTGTACACCCATTAATGTAATTTGCTGGATGACAGATCACTCA	2514
Db	541	AGTGCTACCCATTTACTGTACACCCATTAATGTAATTTGCTGGATGACAGATCACTCA	600
Qy	2515	CATTATATCAGTATTTAGCATCTTGGTGTCTCGGACATCTGCAACAGAGGAGGTATTC	2574
Db	601	CATTATATCAGTATTTAGCATCTTGGTGTCTCGGACATCTGCAACAGAGGAGGTATTC	660
Qy	2575	TTTTCTACTCTGCGTTTCCATCAA	2634
Db	661	TTTTCTACTCTGCGTTTCCATCAA	720
Qy	2635	AGTGCAACTCCCTGGGGTTGTGATGCTGTGCTCGAAAGTCA	2694
Db	721	AGTGCAACTCCCTGGGGTTGTGATGCTGTGCTCGAAAGTCA	780
Qy	2695	GATTATAACTCAGCTGTCCCTACCGGGATGTTAGTGGAGGTTAGGTTTCGACGGCCAG	2754
Db	781	GATTATAACTCAGCTGTCCCTACCGGGATGTTAGTGGAGGTTAGGTTTCGACGGCCAG	840

Qy	2755	TACCACGAAAAGGACCTAGATGTCAACACATTTATTCGGGACTGGGTGGCCAACTACCCA	2814
Db	841	TACCACGAAAAGGACCTAGATGTCAACACATTTATTCGGGACTGGGTGGCCAACTACCCA	900
Qy	2815	GGAGTAGGGGTGGATCTTTTATTTAGACAGCGCGGTATGGTTCTCAGTCTACGGAGGGTTA	2874
Db	901	GGAGTAGGGGTGGATCTTTTATTTAGACAGCGCGGTATGGTTCTCAGTCTACGGAGGGTTA	960
Qy	2875	AAACCCAAATTCACCCAGTGACCTGTACAGAGGGAATATGTATATCAACGGATAC	2934
Db	961	AAACCCAAATTCACCCAGTGACCTGTACAGAGGGAATATGTATATCAACGGATAC	1020
Qy	2935	AATGACACATGCCAGATGAGCAAGACTACACAGATTCGAATGGCAAAGTCTTCTGATAAG	2994
Db	1021	AATGACACATGCCAGATGAGCAAGACTACACAGATTCGAATGGCAAAGTCTTCTGATAAG	1080
Qy	2995	CCTGACCGTTTGGTGGGAAACGCATACAGCAGGCTATCTTATCTATCAAGGTGTCAACA	3054
Db	1081	CCTGACCGTTTGGTGGGAAACGCATACAGCAGGCTATCTTATCTATCAAGGTGTCAACA	1140
Qy	3055	TCCTTAGCGAAGACCCGGTACTGACTGTACCGGCCCAACACAGTCACTCATCGGGGCC	3114
Db	1141	TCCTTAGCGAAGACCCGGTACTGACTGTACCGGCCCAACACAGTCACTCATCGGGGCC	1200
Qy	3115	GAAGGCAAGATTTCTCAGTAGGACATCTCATTTCTTGTATCAACGAGGTCATCATAC	3174
Db	1201	GAAGGCAAGATTTCTCAGTAGGACATCTCATTTCTTGTATCAACGAGGTCATCATAC	1260
Qy	3175	TTCTCTCCCGGTTTATATTCCTATGACAGTACAGCAACAAACAGGCACCTCTTCATAGT	3234
Db	1261	TTCTCTCCCGGTTTATATTCCTATGACAGTACAGCAACAAACAGGCACCTCTTCATAGT	1320
Qy	3235	CCTTATACATTCATGCTTCACTCGGCCAGGTAGTATCCCTTGGCAGGCTTCAGCAAGA	3294
Db	1321	CCTTATACATTCATGCTTCACTCGGCCAGGTAGTATCCCTTGGCAGGCTTCAGCAAGA	1380
Qy	3295	TGCCCCAACTCGTGTGTTACTTGGAGTCTATACAGATCCATATCCCTTAATCTTCTATAGA	3354
Db	1381	TGCCCCAACTCGTGTGTTACTTGGAGTCTATACAGATCCATATCCCTTAATCTTCTATAGA	1440
Qy	3355	AACC 3358	
Db	1441	AACC 1444	

RESULT 12
US-10-725-841-1
; Sequence 1, Application US/10725841
; Publication No. US20040131640A1
; GENERAL INFORMATION:
; APPLICANT: Geerlings, Harmen J.
; APPLICANT: Brown, Ian H.
; APPLICANT: Alexander, Dennis J.
; APPLICANT: Collins, Michael S.
; TITLE OF INVENTION: Escape Mutants of Newcastle Disease Virus as Marker Vaccines
; FILE REFERENCE: AM100044
; CURRENT APPLICATION NUMBER: US/10/725,841
; CURRENT FILING DATE: 2003-12-02
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Paramyxovirus/Newcastle Disease Virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1662)
US-10-725-841-1

Query Match 42.1%; Score 1414; DB 19; Length 1662;
Best Local Similarity 90.7%; Pred. No. 0;
Matches 1507; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

Qy 107 CTGCGACTGAGTTGTCATCTGTCCGGCAAACTCCATTTGATGCGCAGCCCTCTTGACAGTCCA 166
Db 61 CTGCGACTGAGTTGCGTCTGTCCGACAAAGCTCCCTTGTATGGCAGGCCCTCTTGACAGTCCA 120
Qy 167 GGAATTGTGGTTA CAGGAGACAAAGCCGTCAACATATACACCTCATCCGACAGAGATCA 226
Db 121 GGGATTGTGGTGA CAGGAGACAAGAGCAGTCAACATATACACCTCATCTCAGACAGGGTCA 180
Qy 227 ATCATAGTTAGTCTCCCGAATCTGCCAAGATGAAGGAGGATGTGGGAAAGCCCCC 286
Db 181 ATCATAGTCAAGTTACTCCCAAAATATGCCAAGATGAAGAGGGGTGTGCAAAAGCCCCG 240
Qy 287 TTGATGCATACAAACAGACATTGACCACTTTGCTCACCCCCCTTTGCTGACTCTATCCGT 346
Db 241 TTGAGGGGTACAACAGGACATTGACTACTTTGCTCACCCCCCTTTGCTGATTCTATTTCGT 300
Qy 347 AGGATACAAGAGTCTGTGA CTACATCTGGAGGGGGGAGACAGGGGGCGCTTTATAGGGGCC 406
Db 301 AGGATACAAGAGTCTGTGACTACATCTGGAGGGGGAACAGGGGACGCTTTATAGGGGCC 360
Qy 407 ATTATTTGGCGTGGCTCTTGGGGTTGCAACTGCCGCACAAATAACAGCGGCCGACGCT 466
Db 361 ATTATCGCGGTGCAGTCTCGGGGTTGCAACCCGCTGCACAGATAACAGCAGCTTCGGCT 420
Qy 467 CTGATACAAGCCAAACAAAATGCTGCCAACTCCTCCGACTTAAAGAGAGCAATTCGCGCA 526
Db 421 CTGATACAAGCCAAACAAAATGCTGCCAATCCTCCGGCTTAAAGAGAAATTTGCTGCA 480
Qy 527 ACCAATGAGGTGTGCATGAGGTCACTGA CCGATTATCGCAACTAGCAGTGGCAGTTGGG 586
Db 481 ACCAATGAGGTGTGCAGAGTCACTGATGGATTATCACACTAGCAGTGGCAGTTGGG 540
Qy 587 AAGATGACAGCTTTGTTAATGACCAATTAATAAAGCAGCTCAGGAATTAGCTGCATC 646
Db 541 AAGATGACAGCAATTTGTTAATGACAGTTTAATAAAGCAGCTCAGGAATTGGACTGTATA 600
Qy 647 AAAATTGCACAGCAAGTTGGTGTAGAGCTCAACCTGTACCTAACCGAATTCAGCTACAGTA 706
Db 601 AAAATTACCGACAGTTGGTGTAGAACTCAACCTGTATCTAATCTGAATTCAGCTACAGTA 660
Qy 707 TTGCGACACAATAATCACTTCCCTGCTTAAACAGCTGACTATTTCAGGCACTTTACAAT 766
Db 661 TTGCGGCGACAATAATCACTTCCCTGCTTAAACAGCTGACTATCTCCAGGCGCTTTACAAT 720
Qy 767 CTACTGTGGAATATGGAATTAATTTGACTAAGTTAGTGTAGGGAACAATCAACTC 826
Db 721 CTAGTGTGGGAATATGGAATTAATTTGACTAAGTTAGTGTAGGGAACAACAACCTC 780
Qy 827 AGCTCATTAATCGGTAGCGGCTTAATCACCGGTAAACCTTATCTATACGACTCACAGCT 886
Db 781 AGCTCATTAATGGTAGCGGCTGATCACCGGCAACCTTATCTGTAGGACTCACAGCT 840
Qy 887 CAACCTTTGGGTATACAGGTAACCTTCACTTCAGTCGGGAACCTTAATAATATGCGTGC 946
Db 841 CAGCTCTTGGGTATACAGGTAACCTCACTACCTCAGTCGGGAACCTTAATAATATGCGTGC 900
Qy 947 ACCTACTTGGAAACCTTATCGTAAGCACACCGGGATTTGCTCGGCACTTTGCCCA 1006
Db 901 ACCTACTTGGAAACCTTGTCTGTAAAGTACAAACCAAGGATTTGCTCAGCACTCGTCCCA 960
Qy 1007 AAAGTGGTGCACAGGTCGGTCTGTGTATGAAGAACTTGACACTCATACTGTATAGAA 1066
Db 961 AAGTGGTGTATGAAGTTCGGTTCGGTATAGAGAACTTTGACACTCATCTGTATAGAG 1020
Qy 1067 ACTGACTTATGATTTATTTATGTACAGAAATAGTAAGTTCCCTATGTCCCTTGGTATTTAT 1126
Db 1021 ACCGATTTGGATCTATATTGTACAAGAAATAGTGAACATTCCTATGTCTCTCTGGTATTTAT 1080
Qy 1127 TCCTGCTTGAAGGGCAATACGTCGGCTGTATGTACTCAGAGCGAGGGCGCACTTACT 1186
Db 1081 TCCTGTTTGAAGGGCAATACATCGGCTTGGATGTACTCAGAGCTGAAGGGCGCACTACT 1140
Qy 1187 ACACCATACATGACTATCAAGGTTTCAGTCACTCGCCAACTGCAAGATGACAAACATGTAGA 1246

Db 1141 ACGCCGTACATGACTCTCAAAAGGCTCAGTTATTTCCTCAACTGTAAAGATGCAACATGTAGA 1200
Qy 1247 TGTGTAACCCCGCGGTATCATATCGCAAACTATGGAAGAGCGGTGTCTCTAATAAGAT 1306
Db 1201 TGTGCAGACCCCGCGGTATCATATCGCAAAATATGGAAGAGCTGTGTCTCTAATAAGAT 1260
Qy 1307 AAACAATCATGCAATGTTTATCCTTAGGGCGGATAACTTTAAGGCTCAGTGGGGAATTC 1366
Db 1261 AGCAATCATGCAATGTCTTATCCTTAGACGGAATAACTTTGAGGCTCAGTGGGGAATTT 1320
Qy 1367 GATGTAACCTTATCAGAAGAATATCTCAATACAGATTTCTCAAGTAATAATAACAGGCAAT 1426
Db 1321 GATGCAACTTTATCAAAAGAATATCTCAATACAGATTTCTCAAGTAATACTGACAGGCAAT 1380
Qy 1427 CTTGATATCTCACTGAGCTTGGGAATGTCAAACTCGATCAGTAATGCTTTCAATAAG 1486
Db 1381 CTCGATATCTCGACTGAGCTTGGGAATGTCAAACTCGATAGTAATGCTTTAGATAAG 1440
Qy 1487 TTAGAGAAAGCAACAGAAAACTAGACAAAAGTCAATGTCAAACTGACTAGCACATCTGCT 1546
Db 1441 TTAGAGAAAGCAACAGCAAACTAGACAAAGTCAATGTCAAACTGACAGCACATCCGCT 1500
Qy 1547 CTCATTAACCTATATCGTTTGTGACTATCATATCTCTTGTCTTTTGTGTATCTTAGCTGATT 1606
Db 1501 CTCATCACTATATCGTTTAACTGTCTATCTCTTGTGTGTATCTTAGCTGCTT 1560
Qy 1607 CTAGCATGCTACCTAATGTACAGCAAAAGCGCAACAAAAACCTTATTATGCTTTGGG 1666
Db 1561 CTAGCATGCTACCTGATGTACAGCAAAAGCGCAACAGAAAGCTTGTATTATGCTTTGGG 1620
Qy 1667 AATAAATCTCTAGATCAGATCAGAGCCACTACAAAAATGTGA 1708
Db 1621 AATAAATCTCTGATCAGATGAGAGCCACTACGAAATGTGA 1662

RESULT 14
US-09-784-990-10
; Sequence 10, Application US/09784990
; Patent No. US20020037292A1
; GENERAL INFORMATION:
; APPLICANT: AUDONNET, JEAN-CHRISTOPHE
; APPLICANT: BOUCHARDON, ANNABELLE
; APPLICANT: RIVIERE, MICHEL
; TITLE OF INVENTION: AVIAN POLYNUCLEOTIDE VACCINE FORMULA
; FILE REFERENCE: 45413-2260
; CURRENT APPLICATION NUMBER: US/09/784,990
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 96/09339
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: PCT/FR97/01326
; PRIOR FILING DATE: 1997-07-16
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Newcastle disease virus
US-09-784-990-10

Query Match 40.6%; Score 1362.8; DB 9; Length 1662;
Best Local Similarity 88.7%; Pred. No. 0;
Matches 1475; Conservative 0; Mismatches 187; Indels 0; Gaps 0;

Qy 47 ATGGGCTCCAGACCTTCTACCAAGAACCCAGCACCTATGATGCTGACTATCCGGTTGCG 106
Db 1 ATGGGCTCCAGATCTTCTACCCAGGATCCCGGTACCTCTAATGCTGAATCATCCGAACCCGCG 60
Qy 107 CTGCGACTGAGTTGCTCATCTGTCCGGCAAACTCCCAATTGATGGCAGGCCCTCTTTCAGCTGCA 166
Db 61 CTGACACTGAGCTGTATCCGCTCTCAGCAAGCTCTCTTGTATGGCAGGCCCTCTTTCGGGCTGA 120
Qy 167 GGAATTGTGGTTACAGGAGACAAAGCCGCTCAACATATACACTCATCCAGACAGGATCA 226

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Db 121 GGGATCGTGGTAAAGGAGATAAGCAGTCAACATATACACTCATCCATCCAGACAGCGTCA 180
Qy 227 ATCATAGTAAAGCTCCTCCGAATCTGCCAAGATAAGAGGACATGTGCGAAAGCCGCC 286
Db 181 ATCATAGTAAAGTAACTCCGAATATGCCAAGGACAAAGAGGTGTGTGCAAAAGCCCCA 240
Qy 287 TTGGATGATACAAACAGACATATGACCACTTGGCTCACCCCGCTTGGTGACTCTATCGGT 346
Db 241 TTGGAGGATACAAACAGACATGACTACTTTACTCACCCCGCTTGGTGATTTCTATCCGC 300
Qy 347 AGGATACAAGAGTCTGTGACTACATCTGAGGGGGAGACAGGGCGCTTATAGCGCC 406
Db 301 AGGATACAAGAGTCTGTGACTACTTCCGAGGAGAGACAGAGACGCTTTATAGTGCC 360
Qy 407 ATTATTTGGCGGTGGCTCTTGGGGTTGCAACTGCCGACCAATAACAGCGCGCCAGCT 466
Db 361 ATTATCGCGAGTGTAGCTCTTGGGGTTGGACAGCTGCACAGATAACAGCAGCTTCGGCC 420
Qy 467 CTGATACAAGCCAAACAAATGCTGCCAATCTCCGACATCTCCGACTTAAAGAGAGCATTCGCCGA 526
Db 421 CTGATACAAGCCAAACAGAACTGCTGCCAATCTCCGCGCTTAAAGAGAGCATTTGCTGCA 480
Qy 527 ACCAATGAGGCTGTGCATGAGTCACTGACCGATTTATCGCACTAGCAGTGGCAGTTGGG 586
Db 481 ACCAATGAGCTGTGCACAGGTCACTGACCGATTTATCAAACTAGCAGTGGCAGTAGGG 540
Qy 587 AAGATGACAGCAGTTTGTAAAGACCAATTTAATAAAACAGCTCAGGAATTAAGACTGCATC 646
Db 541 AAGATGACACAGTTTGTCAATGACCAAGTTCAATAATACAGCGCAAGAAATGGAGCTGATA 600
Qy 647 AAAATTGCACAGCAAGTTGGTGTAGAGCTCAACCTGTATCCTTAACCGAATTAAGTACAGTA 706
Db 601 AAAATTGCACAGCAGGTCCGTGTAGAACTCAACTTGTACTCACTAACTGAATTAAGTACAGTA 660
Qy 707 TTGCGACACAAATCACTCACTGCTTTAAACAGCTGACTATTTCAGGCACTTTACAAAT 766
Db 661 TTGCGCCACAAATCACTTCCCTGCTTAACTGAGCTGACTATCAAGCGCTTTACAAAT 720
Qy 767 CTAGCTGGTGAATATGATTTACTTTTACTAAGTGTAGGTAGGGAACAAATCAACTC 826
Db 721 CTAGCTGGTGAATATGATTTACTTTGCTGACTAAGTGTAGGTAGGGAACAACTC 780
Qy 827 AGCTCAATTAAGTGTAGGCTTAATACCGGTAAACCTATTCTATACAGCTCACAGACT 886
Db 781 AGCTCAATTAAGTGTAGGCTTGATCACCGGCAACCTATTCTGTAGCACTCACAGACT 840
Qy 887 CAACCTTTGGGTATACAGTAACTCTACTTCAGTCCGGACCTAAATAATATGCGTCC 946
Db 841 CAGATCTTTGGGTATACAGTAACTTTGCTTCAGTTGGGAACCTGAATAATATGCGTCC 900
Qy 947 ACCTACTTTGGAAACCTTATCCGTAAAGCAACACCGGGAATTTGCTCCGCACTTGTCCCA 1006
Db 901 ACCTACTTTGGAGACCTTATCTGTAAAGCAACACCAAGGATTTGCTCAGCACTTGTCCCA 960
Qy 1007 AAAGTGTGACACAGGTCCGTCTGTGTATAGAGAACTTGACACTCATACTGTATAGAA 1066
Db 961 AAAGTGTGACACAGGTCCGTTCGTGTATAGAGAACTTGACACTCATACTGTATAGG 1020
Qy 1067 ACTGACTTATGATTTATATGTACAGAAATAGTAAGCTTCCCTATGTCCTCCCTGGTATTTAT 1126
Db 1021 ACCGACTTGGATTTATATCTGTAACAAGAAATAGTGACATTTCCCTATGTCCTCCCTGGTATTTAT 1080
Qy 1127 TCCTGCTTGGCGGCAATGACGCGCTGTATGTACTCAAGACCGAAGGCGCACTTACT 1186
Db 1081 TCTGTCTGAGCGGTAATATACATCGGCTTGCAATGTTCAAGACTGAAGGCGCACTTACT 1140
Qy 1187 ACACCATATGACTATCAAAAGGTTTCACTCATCGCCAACTGCAAGATGACAACTGTAGA 1246
Db 1141 ACGCCATATATGGCTCTCAAGGCTCAGTTATTTGCAATTTGCAATTTGCAACATGTAGA 1200
Qy 1247 TGTGTAAACCCCGGGTATCATATTCGCAAACTATAGGAGAGCGGTGTCTCTAATAGAT 1306
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Db 1201 TGTGAGATCCCCCAGGTATCATATCGCAAAATATATGGAGAGCTGTGTCTTAAATAGAT 1260
Qy 1307 AAAACAATCATGCAATGTTTTTATCTTATAGCGGGATAAACTTTTAAAGCTCAGTGGGAAATTC 1366
Db 1261 AGGCACTCATGCAACGTCTTATCTTATAGCGGATAAACTCTGAGGCTCAGTGGGAAATTT 1320
Qy 1367 GATGTAACCTTATCAGAAGAATATCTCAATACAAGATTCTCAAGTAATATATACAGCAAT 1426
Db 1321 GATGCAACCTATCAAAAGAATATCTCTATATCTAGATTCTCAAGTTTATAGTGACAGCAAT 1380
Qy 1427 CTTGATATCTCAACTGAGCTTGGGAATGTCAACAACTCGATCAGTAAATGCTTTTGAATAAG 1486
Db 1381 CTTGATATCAACTGAGCTTGGGAATGTCAACAACTCAATAAGTAATGCTTGAATAAG 1440
Qy 1487 TTAGAGAAAGCAACAGAAACTAGACAAAGTCAATGTCAAACTGACATAGCACTCTGCT 1546
Db 1441 TTAGAGAAAGCAACAGCAAACTAGACAAAGTCAATGTCAAACTGACAGCACTCTGCT 1500
Qy 1547 CTCATTACCTATATCGTTTTGACTATCATATCTCTGTTTTTGGTATATCTTACGCTGATT 1606
Db 1501 CTCATTACCTATATCGTTTTTAACTGTCTATCTCTGTTTTTGGTGTACTTTAGCCCTGGT 1560
Qy 1607 CTAGCATCTACCTAAATGTACAAGCAAAAGCGCAACAAACCTTATTATGGCTTGGG 1666
Db 1561 CTAGCATCTACCTGATGTACAGCAAAAGGCAACAAAGACCTTGTATGGCTTGGG 1620
Qy 1667 AATAATCTCTAGATCAGATGAGAGCCACTCAAAAAATGTGA 1708
Db 1621 AATAATACCTTGATCAGATGAGAGCCACTCAAAAAATATGA 1662
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RESULT 15

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US-10-229-412-10
; Sequence 10, Application US/10229412
; Publication No. US20030124145A1
; GENERAL INFORMATION:
; APPLICANT: AUDONNET, JEAN-CHRISTOPHE
; APPLICANT: BOUCHARDON, ANNABELLE
; APPLICANT: RIVIERE, MICHEL
; TITLE OF INVENTION: AVIAN POLYNUCLEOTIDE VACCINE FORMULA
; FILE REFERENCE: 454313-2260
; CURRENT APPLICATION NUMBER: US/10/229,412
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US/09/232,479
; PRIOR FILING DATE: 1999-01-15
; PRIOR APPLICATION NUMBER: 96/09339
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: PCT/FR97/01326
; PRIOR FILING DATE: 1997-07-16
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Newcastle disease virus
US-10-229-412-10
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Query Match 40.6%; Score 1362.8; DB 15; Length 1662;
Best Local Similarity 88.7%; Pred. No. 0;
Matches 1475; Conservative 0; Mismatches 187; Indels 0; Gaps 0;
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Qy 47 ATGGGCTCCAGACCTTCTTACCAAGAACCCAGCACTATGATGCTGCTATCCGGGTGG 106
Db 1 ATGGGCTCCAGATCTTCTACCAAGATCCCGGTACCTCTAATGCTGATCATCCGAACGCG 60
Qy 107 CTGGCACTGAGTGTGATCTGTCCGCAAACTCCATTGATGGCAGGCTCTTGCAGTCA 166
Db 61 CTGACACTGAGCTGTATCCGTCTGACAAAGCTCTCTTGTATGGCAGGCTCTTTCGGCTGCA 120
Qy 167 GGAATTGTTGTATACAGGAGACAAAGCCCTCAACATATACACCTCATCCAGACAGATCA 226
Db 121 GGGATCGGTGAACAGGAGATAAGCAGTCAACATATACCTCATCCAGACAGGCTCA 180
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QY 227 ATCATAGTTAAGCTCTCCCGAATCTGCCAAGATTAAGGAGGCATGTGGAAAGCCCC 286
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QY 287 TTGGATCATACAAACAGACANATGACCACTTTTGCTCAACCCCTTTGGTGACTCTATCCGT 346
Db 241 TTGGAGGCATACAAACAGACACACTGACTACTTTTACTCACCCCTTTGGTGATTTCTATCCGC 300
QY 347 AGGATACAAGAGTCTGTGACTACATCTGGAGGGGAGACAGGGCGCCCTTATAGGCGCC 406
Db 301 AGGATACAAGAGTCTGTGACTACTTCCGGAGAGAGAGACAGAGCCCTTTATAGGTGCC 360
QY 407 ATTATGGCGTGTGGCTCTTGGGGTTGCAACTGCCGCAAAATAACAGCGCGCCGACGCT 466
Db 361 ATTATCGCAGTGTAGCTCTTGGGGTTGCGNACAGCTGCACAGATAACAGCAGCTTCGGCC 420
QY 467 CTGATACAAGCCAAACAAAATGCTTGCCAAACATCTCCGACTTAAAGAGAGCAATTCGCCGA 526
Db 421 CTGATACAAGCCAAACAGNATGCTTGCCAAACATCTCCGGCTTAAAGAGAGCAATTCGTGCA 480
QY 527 ACCAATGAGGCTGTGCATGAGGTCACTGACGGATTATCGNACTAGCAGTGGCAGTTGGG 586
Db 481 ACCAATGAGCTGTGCAGAGGTCACCTGACGGATTATCACAACCTAGCAGTGGCAGTAGGG 540
QY 587 AAGATGACAGAGTTTGTGTAATGACCAATTTAATAAAGCAGCTCAGGAATTAGACTGCATC 646
Db 541 AAGATGCAACAGTTTGTTCNATGACAGTTCNATTAATACAGGCGCAAGATTGGACTGTATA 600
QY 647 AAAATTGCACAGCAAGTTGGTGTAGAGCTCAACCTGTACTTAACCGAATTGACTACAGTA 706
Db 601 AAAATTGCACAGCAGGTCGGTGTAGAACTCAACTTGTACTTAACCGAATTGACTACAGTA 660
QY 707 TTCCGACCAAAATCACTTCACTGCTTTAAACAGCTGACTATTTCAGGCACCTTTACAAT 766
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QY 767 CTAGCTGTGGAAATATCGAATTACTTTATGTAAGTGTAGGTAGGGAAACAATCAACTC 826
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QY 947 ACCTACTTTGGAAACCTTATCGTAAAGCAACACCGGGATTTGCTCGGCACTTTGTCCCA 1006
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QY 1007 AAAGTGGTGACACAGGTCGGTCTTGTGTAGAGAACTTGAACCTCATACTGTATAGAA 1066
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QY 1127 TCCTGCTTGGCGGCAATACGTGCGCTGTATGTACTCAAGACCGAAGGCGCACTTACT 1186
Db 1081 TCTTGTCTGAGCGGTAATACATCGGCTTGCAATGTATTTCAAGACTGAAGGCGCACTTACT 1140
QY 1187 ACACCATACATGACTATCAAGGTTTCACTGCTCGCCAACTGCAAGATGACCAACATGTAGA 1246
Db 1141 ACGCCATATATGGCTCTCAAGGCTCAGTTATTGCCAAATGCAAGCTGCAACAATGTAGA 1200
QY 1247 TGTGTAAACCCCGGTTATCATATCGCAAACTATGGAGAGCGGTCTCTAATAGAT 1306
Db 1201 TGTGCAGATCCCCAGGTATCATATCGCAAAATTTATGGAGAGCTGTGTCTCTTATAGAT 1260
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Db 1261 AGGCACCTCATGCAACGCTCTTTATCTTTAGACGGGATAAATCTTGAGGCTCAGTGGGAATTT 1320
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Db 1321 GATGCAACCTTATCAAAAGAATATCTCTATACTAGATTCTCAAGTTATAGTGACAGGCAAT 1380
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Db 1381 CTTGATATATCAACTGAGCTTTGGGAATGTCAA CAACCTCAATAAGTAATGCCCTGAATAAG 1440
QY 1487 TTAGAGAAAGCAACAGAAACCTAGACAAAGTCAATGTCAAACTGACTAGCACATCTGCT 1546
Db 1441 TTAGAGAAAGCAACAGCAAACTAGACAAAGTCAATGTCAAACTGACCAGCACATCTGCT 1500
QY 1547 CTCAATTACCTATATCGTTTTTGACTATCATATCTCTTGTGTTTTTGTGTATCTTAGCCTGATT 1606
Db 1501 CTCAATTACCTATATCGTTTTTAACTGTCAATATCTCTTGTGTTTTTGTGTACTTAGCCTGTT 1560
QY 1607 CTAGCATGCTACCTTAATGTACAAGCAAAAGCGCAACAAAAACCTTTATTTATGCTTTGGG 1666
Db 1561 CTAGCATGCTACCTGATGTACAAGCAAAAGCGCAACAAAAAGACCTTTGTTTATGCTTTGGG 1620
QY 1667 AATAAATCTCTAGATCAGATGAGGCCACTACAAAAATGTGA 1708
Db 1621 AATAAATACCTTGTATCAGATGAGGCCACTACAAAAATATGA 1662
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Search completed: October 1, 2005, 19:23:23

Job time : 2151 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 1, 2005, 11:19:28 ; Search time 10319 Seconds
(without alignments)
12386.841 Million cell updates/sec

Title: US-10-800-256-1
Perfect score: 3358
Sequence: 1 acgggtagaagattcttgat.....cctaattcttatagaaacc 3358

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hcc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	500.8	14.9	766	CK280174	SSH227 SS
2	87.8	2.6	692	BG661033	BG661033 N339 SSH-
3	46.2	1.4	862	AZ538746	AZ538746 ENTDM69TF
4	46.2	1.4	886	AZ541254	AZ541254 ENTFAL1TF
5	43.6	1.3	406	AY032979	AY032979 AY032979
6	43.2	1.3	386	AW329422	AW329422 NZ00657e
7	43.2	1.3	494	AL380807	AL380807 MCB854F09
8	43.2	1.3	670	BF641250	BF641250 NF058C11
9	42.6	1.3	1022	AL257280	AL257280 Tetraodon
10	42.4	1.3	507	CD081007	CD081007 MA3-9995U
11	42.4	1.3	816	BH183366	BH183366 Q23_G14-
12	42.4	1.3	816	AL620307	AL620307 T7 end of
13	42	1.3	651	CK335184	CK335184 H3150E07-
14	42	1.3	687	BY732720	BY732720 BY732720
15	42	1.3	719	BM950384	BM950384 UI-N-EHOp
16	42	1.3	751	CL797382	CL797382 OR_Cha000
17	41.8	1.2	1085	AL101102	AL101102 Drosophil
18	41.6	1.2	845	AL053138	AL053138 Drosophil
19	41.4	1.2	1101	AL078714	AL078714 Drosophil
20	41.2	1.2	422	BU496251	BU496251 PfESToac0
21	41.2	1.2	847	AL053305	AL053305 Drosophil
22	41	1.2	893	BH150882	BH150882 ENTPT21TR
23	40.8	1.2	1079	BX375722	BX375722 BX375722
24	40.6	1.2	716	CE672698	CE672698 tigr-gss-

25 40.4 1.2 670 8 BH158224 ENTSP70TF
c 26 40.4 1.2 714 8 AQ324694 mgx00019D
c 27 40.4 1.2 801 9 BX213898 Danio rer
c 28 40.2 1.2 779 8 AQ855008 CpG2055B
c 29 40.2 1.2 865 8 BH180441 016_H_20-
c 30 40.2 1.2 865 9 CNS07WAN T3 end of
c 31 40.2 1.2 878 9 CNS0187R Drosophil
c 32 40.2 1.2 1101 9 CNS003FR AL064653 Drosophil
c 33 40 1.2 529 9 CC853182 CC853182 NDL.12651
c 34 40 1.2 1032 9 CNS01ONH AL099191 Drosophil
c 35 40 1.2 1086 9 CNS00YXK AL096962 Drosophil
c 36 39.8 1.2 434 4 BJ423154 BJ423154
c 37 39.8 1.2 516 7 CO189289 CO189289 EK043805
c 38 39.8 1.2 584 9 CR484222 CR484222 Medicago
c 39 39.8 1.2 688 9 CG945897 CG945897 MBE1M966R
c 40 39.8 1.2 740 9 CG943717 CG943717 MBEAD92TR
c 41 39.8 1.2 764 9 CG932090 CG932090 MBECA44TR
c 42 39.8 1.2 868 9 CG924570 CG924570 MBEAB79TR
c 43 39.6 1.2 567 9 CR346391 CR346391 Medicago
c 44 39.6 1.2 580 8 AZ583873 AZ583873 1M0388J04
c 45 39.6 1.2 913 9 CNS04HG7 AL290896 Tetraodon

ALIGNMENTS

RESULT 1
CK280174 766 bp mRNA linear EST 05-JAN-2004
LOCUS SSH227 SSH generated forward (3 days-2 days) subtracted cDNA
DEFINITION Library Phanerochaete chrysosporium cDNA, mRNA sequence.
ACCESSION CK280174
VERSION CK280174.1 GI:40556623
KEYWORDS EST.
SOURCE Phanerochaete chrysosporium (anamorph: Sporotrichum pruinosum)
ORGANISM Phanerochaete chrysosporium
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Ascomycota; Basidiomycota; Corticiales; Phanerochaete.
REFERENCE 1 (bases 1 to 766)
AUTHORS Jiang,M. and Zhang,Y.
TITLE Screen for Temporal-specific Expression Genes of Phanerochaete
chrysosporium Based on SSH and cDNA Microarrays
JOURNAL Unpublished (2003)
COMMENT Contact: Yizheng Zhang
Sichuan Key Laboratory of Molecular Biology and Biotechnology
College of Life Science, Sichuan University
Chengdu, Sichuan, box610064 P.R.CHINA
Tel: 86 028 85412738
Email: yizhang@scu.edu.cn

SSH generated forward (3 days-2 days) subtracted cDNA library of
Phanerochaete chrysosporium; average insert size:600 bp;
information: Isolation of total RNA from the mycelia incubated in
shallow stationary culture (Kirk media) at 39_

FEATURES

Location/Qualifiers
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/organism="Phanerochaete chrysosporium"
/mol_type="mRNA"
/strain="BKM-F-1767"
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source
SSH generated forward (3 days-2 days) subtracted cDNA library of
Phanerochaete chrysosporium; average insert size:600 bp;
information: Isolation of total RNA from the mycelia incubated in
shallow stationary culture (Kirk media) at 39_

ORIGIN

Query Match 14.9%; Score 500.8; DB 7; Length 766;
Best Local Similarity 84.1%; Pred. No. 7.4e-137;
Matches 565; Conservative 0; Mismatches 107; Indels 0; Gaps 0;
QY 43 CAAGATGGGCTCCAGACCTTCTTACCAAGACCACCTATGATGCTATCGGGT 102

Db 95 CACCATGGCTCCAAACTTCTACAGGATCCGAGCACTCTGATGTGATCATCCCGGAT 154
Qy 103 TGCCTGGCACTGAGTTGCTATCTGTCGGGAAATCTCCATGATGCGAGGCTCTTTGAGC 162
Db 155 TATGCTGATATTGGCTGATCCGTCGACAAAGCTCTCTTGACGGCAGGCTCTTTGAGC 214
Qy 163 TGCAGGAATTGTTGTACAGAGACAAAGCGCTCAATATATACACTCTATCCGAGAG 222
Db 215 TGCAGGAATTGTTGTACAGAGATAAGGCACTCAATGTATACACTCTGTTCTCAGAG 274
Qy 223 ATCAATCATAGTTAAGCTCTCCGAACTCTCCCAAGGATAAGGAGGATGTGGAAGC 282
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Qy 403 CGCCATTATTGGCGGTGGCTCTTGGGGTTGCAACTGCCGACAAATAACAGGGCGC 462
Db 455 TGCTGTTATTGGCGGTGAGTCTTGGGTTGCAACAGCGGACAGATAACAGAGTGC 514
Qy 463 AGCTCTGATACAGCCAAACAAATGTGCAACATCTCCGACTTAAAGAGAGCATTC 522
Db 515 GGCCCTAATACAGCCAAACCGAATGCCGCAACATCTCCGGCTTAAGGAGAGCATTC 574
Qy 523 CGCAACCAATGAGGCTGTGATGAGTCACTGACGGATTTATCGCACTAGCAGTGGCAGT 582
Db 575 TGCAACCAATGAAGCTGTGATGAAGTCAACGACGCGATTTATCGCACTATCAGTGGCAGT 634
Qy 583 TGGGAAGATGAGCAGGTTTGTATGACCAATTTAATAAAGACAGTCAAGGAATTAGACTG 642
Db 635 TGGGAAGATGAGCAGGTTTGTATGACCAATTTAATAAAGACAGGCGGAGAAATTGGACTG 694
Qy 643 CATCAAAATTGCACAGCAAGTTGTTGATAGACTCAACCTGTACCTAACCCGAATTGACTAC 702
Db 695 TATRAAATACACAAACAGGTTGTTGATAGAACTCAACCTATACCTAACTGAATTGACTAC 754
Qy 703 AGTATTCGGACC 714
Db 755 AGTATTCGGGCC 766

RESULT 2
BG661033
LOCUS N339 SSH-HCA-U library Homo sapiens cDNA, mRNA linear EST 26-APR-2001
DEFINITION
ACCESSION BG661033
VERSION BG661033.1 GI:13805211
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Zhang,Z. and DuBois,R.N.
TITLE Detection of differentially expressed genes in human colon cancer cells treatment with NS-398 using suppression subtractive hybridization and differential screening
JOURNAL Unpublished (2000)
COMMENT Contact: Zhonghua Zhang
Department of Medicine
Vanderbilt Medical Center
MCN C-2104, 1161 21st Ave. South, Nashville, TN 37212, USA
Tel: 615 343 1369
Fax: 615 343 6229
Email: zhonghua.zhang@mcmail.vanderbilt.edu
DNA sequencing by: Vanderbilt Medical Center DNA sequencing core

laboratory. This is a fragment of gene that up-regulated by NS-398 treatment.
PCR Primers
FORWARD: 5'-CTAATAGCACTACTATAGGC-3'
BACKWARD: 5'-TCGAGCGCCGCGGCGAGGT-3'
Seq primer: M13 forward primer
High quality sequence stop: 692.
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source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_type="Colon cancer cell"
/cell_line="HCA-7"
/clone_lib="SSH-HCA-U library"
/notes="Vector: PCR2.1-TOPO; Poly A RNA was isolated from NS-398 treated and control cells, and suppression subtractive hybridization was performed in forward and reverse directions. The adapter sequences used in the hybridization were as follows:
5'-CTAATAGCACTACTATAGGCCTCGAGCGCGCCCGGCGAGGT-3'
(adapter 1) and
5'-CTAATAGCACTACTATAGGCAGCGTGTGCGGCGCAGGT-3' (adapter 2)."

ORIGIN
Query Match 2.6%; Score 87.8; DB 4; Length 692;
Best Local Similarity 48.7%; Pred. No. 6.3e-14;
Matches 273; Conservative 0; Mismatches 282; Indels 6; Gaps 1;
Qy 219 CAGGATCAATCATAGTTAAGCTCTCCGAACTCTGCCAAGGATAAGGAGCATGTGCGA 278
Db 132 CAGCATTCATTTGTTGAAGTTAATGCTCAATGACTGCCGATTTAGTGTGATTAATA 191
Qy 279 AAGCCCCCTTTGGATGCATACAAAGGACATTTGCTCACCCTCTTGGTGAAT 338
Db 192 TAACATCAATTTCAAGCTATAATGCAACAGTGACAAACCTCTACAGCGATCGTGAGA 251
Qy 339 CTATCCGTAGATACAAAGTCTGTGACTACATCTGAGGGGGGAGACAGGGGCGCTTA 398
Db 252 ATTTGGAGACAATTTAGGAACCGATTGATTCCACT-----CGGAGGAGACGCCGATTG 305
Qy 399 TAGCGCCCATTTATTGGCGGTGTGGCTCTTGGGGTTGCAACTGCCGCAAAATAACAGCGG 458
Db 306 CAGGGGTGTTGATTGGATTAGTCTGATTTAGGATGAGTACTGCCGACAGCTCACTGCCG 365
Qy 459 CCGCAGCTCTGATACAAAGCCAAACAAATGCTGCCAATCTCTCCGACTTAAAGAGAGCA 518
Db 366 CAGTAGCACTAGTAAAGGCAAAATGAAATGCTGGCGCTACTCAATCTCAAAATGCAA 425
Qy 519 TTGCCGCAACCATGAGGCTGTGATGAGTCACTGAGGATTTATCGCACTAGCAGTGG 578
Db 426 TCCAAAAACAAATGCGGCAAGTTTCAGACGTTGTCAGAGGCCACAAATCACTAGAAACGG 485
Qy 579 CAGTTGGGAAGATGACGACAGTTTCTTAATGACCAATTTAATAAAGACAGCTCAGGAATTAG 638
Db 486 CAGTTCAAGCAGTTCAAGATCATATAACAGTTGGTGAAGTCCAGCAATTTACAGAGCCA 545
Qy 639 ACTGCATCAAAATTTGCACAGCAAGTTGGTTAGAGCTCAACCTGTACTACCTAACCGAATTGA 698
Db 546 ACTGTAAGGCCCAAGATGCTATCATTTGGCTCAATCTCAATCTCTATTGACCGAGTTGA 605
Qy 699 CTACAGTATTTCGACCAACCAATCACTTCACTGCTTTTAAACAAGCTGACTATTTAGGCAC 758
Db 606 CAACTATCTTCCACAATCAAAATTAACAAACCTGCAATTTAGTCTTATTACAAATTTCAAGCTT 665
Qy 759 TTTACAACTAGCTGTTGGA 779
Db 666 TAAGGATTCTACTGGGAGTA 686
RESULT 3
AZ538746/c

LOCUS AZ538746 862 bp DNA linear GSS 14-NOV-2000
 DEFINITION ENTDM6STF Entamoeba histolytica Sheared DNA Entamoeba histolytica genomic, genomic survey sequence.

ACCESSION AZ538746
 VERSION AZ538746
 KEYWORDS AZ538746.1 GI:11143976
 SOURCE GSS.
 ORGANISM Entamoeba histolytica
 Entamoeba histolytica
 Eukaryota; Entamoebidae; Entamoeba.

REFERENCE 1 (bases 1 to 862)
 AUTHORS Loftus,B., Van Aken,S. and Fraser,C.
 TITLE Determination of clone end sequences from Entamoeba histolytica
 HMI:IMSS sheared DNA library

JOURNAL Unpublished (2000)
 COMMENT Contact: Brendan J Loftus
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0208
 Fax: 301 838 3543
 Email: bjlloftus@tigr.org
 Clones are derived from the Entamoeba histolytica HMI:IMSS sheared DNA library

Seq primer: M13-Forward
 Class: shotgun
 High quality sequence start: 36
 High quality sequence stop: 832.
 Location/Qualifiers

FEATURES
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 /note="Vector: pHOS1; Site 1: Bst I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD.
 Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a tight size distribution (~2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999)."

ORIGIN
 Query Match 1.4%; Score 46.2; DB 8; Length 862;
 Best Local Similarity 52.8%; Pred. No. 0.17;
 Matches 123; Conservative 0; Mismatches 108; Indels 2; Gaps 1;
 QY 1449 GGAATGTCACAACTCGATCAGTAATGCTTTGAATAAGTTAGAGAAAGCAACAGAAAC 1508
 Db 771 GGAATAACTACCAACCAATGAAATAATATTTTATTAAAT--GGACAAATAAATCAATA 714
 QY 1509 TAGACAAAGTCAATGTCAAACCTAGCAGCATCTGCTCTCATTCACCTATATCGTTTGA 1568
 Db 713 GTGTAATATTAGAAATTAATCAAAAATAACATATGGAATAATTTATCTTATGTTTAA 654
 QY 1569 CTATCATATCTCTTTGTTGGTATACCTAGCCGTGATTCAGCATGCTACCTAATGTACA 1628
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 QY 1629 AGCAAAAGCGCCACAAAACCTTTATATGGCTTGGGAATAAATCTCTAGAT 1681
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RESULT 4
 AZ541254/c
 LOCUS 886 bp DNA linear GSS 14-NOV-2000

DEFINITION ENTFAITTF Entamoeba histolytica Sheared DNA Entamoeba histolytica genomic, genomic survey sequence.

ACCESSION AZ541254
 VERSION AZ541254.1 GI:11148809
 KEYWORDS GSS.
 SOURCE Entamoeba histolytica
 Entamoeba histolytica
 Eukaryota; Entamoebidae; Entamoeba.

REFERENCE 1 (bases 1 to 886)
 AUTHORS Loftus,B., Van Aken,S. and Fraser,C.
 TITLE Determination of clone end sequences from Entamoeba histolytica
 HMI:IMSS sheared DNA library

JOURNAL Unpublished (2000)
 COMMENT Contact: Brendan J Loftus
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0208
 Fax: 301 838 3543
 Email: bjlloftus@tigr.org
 Clones are derived from the Entamoeba histolytica HMI:IMSS sheared DNA library

Seq primer: M13-Forward
 Class: shotgun
 High quality sequence start: 27
 High quality sequence stop: 842.
 Location/Qualifiers

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 /note="Vector: pHOS1; Site 1: Bst I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD.
 Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a tight size distribution (~2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999)."

ORIGIN
 Query Match 1.4%; Score 46.2; DB 8; Length 886;
 Best Local Similarity 52.8%; Pred. No. 0.17;
 Matches 123; Conservative 0; Mismatches 108; Indels 2; Gaps 1;
 QY 1449 GGAATGTCACAACTCGATCAGTAATGCTTTGAATAAGTTAGAGAAAGCAACAGAAAC 1508
 Db 568 GGAATAACTACCAACCAATGAAATAATATTTTATTAAAT--GGACAAATAAATCAATA 511
 QY 1509 TAGACAAAGTCAATGTCAAACCTAGCAGCATCTGCTCTCATTCACCTATATCGTTTGA 1568
 Db 510 GTGTAATATTAGAAATTAATCAAAAATAACATATGGAATAATTTATCTTATGTTTAA 451
 QY 1569 CTATCATATCTCTTTGTTGGTATACCTAGCCGTGATTCAGCATGCTACCTAATGTACA 1628
 Db 450 CAATATTAAATTTATTTCTTAATTAACAATTTGGAATGTTTATTGTAATATACAGATTATA 391
 QY 1629 AGCAAAAGCGCCACAAAACCTTTATATGGCTTGGGAATAAATCTCTAGAT 1681
 Db 390 ATAAAGAAAGAAAGATAAATTAAGAGTGGATTAAATTAATCAATTATAT 338

RESULT 5
 AY032979/c
 LOCUS 406 bp mRNA linear EST 03-MAY-2002
 DEFINITION AY032979 upregulated by angiotensin II in mesangial cells Homo

sapiens cDNA clone Angrgm-52f, mRNA sequence.

ACCESSION AY032979
VERSION AY032979.1 GI:20429781

KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 406)

Zhou, A., Zhang, H. and Wang, H.

Cloning and identification of a novel gene up-regulated in human mesangial cells stimulated by angiotensin II

Unpublished (2002)

Contact: Zhou, A., Zhang, H. and Wang, H.

Institute of Nephrology

Peking University

No. 8, Xishiku St., Beijing, 100034, P. R. China.

FEATURES

source 1..406
Location/Qualifiers
1..406
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="Angrgm-52f"
/clone_lib="upregulated by angiotensin II in mesangial cells"

ORIGIN

Query Match 1.3%; Score 43.6; DB 2; Length 406;
Best Local Similarity 47.2%; Pred. No. 0.74;
Matches 133; Conservative 0; Mismatches 149; Indels 0; Gaps 0;

QY 401 GCGCCATTATTCGGGTGGCTCTTGGGTTGCACTGCCGACAAATAACAGCGCC 460
|||
Db 282 GGGCGGTCTATCGGTGGATTAGGGTGGCGACTTCAGCGCAGATTACAGCGC 223
|||
QY 461 GCAGCTCTGATACAAGCCAAACAAATGCTGCCAACATCTCCGACTTAAAGAGAGCAT 520
|||
Db 222 GTTGTCTTCACAACTCCATTCAGAAATGCAATGCTATTGTGACACTCAAGATTCTATC 163
|||
QY 521 GCGCAACCAATAGGCTGTGCATGAGGTCACTGACGGATTATCGCAACTAGACGTGCA 580
|||
Db 162 AGGCAGTCTAACAAAGCAATACAGAATTACAAACAGCTATGTCTACCACTGTGCTGTG 103
|||
QY 581 GTTGGGAAGATGCGACAGTTGTTAATGACCAATTTAATAAACAGCTCAGGAATTAGAC 640
|||
Db 102 TTAATGCTCTCCAGGACCGAGATAAATACAGTTGCCCCAGCTATAAATTCCTAGGA 43
|||
QY 641 TGCATCAAAATTGCACAGCAAGTTGGTGTAGAGCTCAACCTG 682
|||
Db 42 TGCAGGTGGTTGCTAATACACTAGGTCTAAATTAACACAG 1
|||

RESULT 6

AW329422
LOCUS AW329422
DEFINITION N200657e rootphos(-) Medicago truncatula cDNA clone MHRP-19H9, mRNA sequence.

ACCESSION AW329422

VERSION AW329422.1 GI:6800017

KEYWORDS EST.

SOURCE Medicago truncatula (barrel medic)

ORGANISM Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.

1 (bases 1 to 386)

Harrison, M.J., Liu, J., Harris, A.R., Scott, A.D., Gonzales, R.A.,

Gonzales, M.B. and Ellis, L.

ESTs from phosphate starved roots

Unpublished (1999)

Contact: Harrison M.J.

Plant Biology Division

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73401

Tel: 580-223-5810

Fax: 580-221-7380

Email: mjharrison@noble.org

Date: 1/23/00; updated to the Database of Expressed Sequence Tags (dbEST) on 04/27/00; More information is available at 'http://chrysis.tamu.edu/medicago'.

Seq primer: T3.

FEATURES

source

Location/Qualifiers

1..386

/organism="Medicago truncatula"

/mol_type="mRNA"

/cultivar="Jemalong, line A17"

/db_xref="taxon:3880"

/clone="MHRP-19H9"

/tissue_type="roots"

/dev_stage="phosphate starved"

/clone_lib="rootphos(-)"

/notes="Vector: pBluescript SK -; Site 1: EcoRI; Site 2: XhoI; At the trifoliolate stage, M. truncatula plants were

transplanted to phosphate-free sand and grown for a

further 30 days. During this 30 day period, they were

fertilized twice weekly with 1/2 Hoaglands solution

containing only 20uM potassium phosphate. RNA was prepared

from the roots. cDNA was prepared from polyA+ enriched

RNA. The cDNA was directionally ligated into the Unizap XR

vector from Stratagene and packaged using Gigapack III

Gold packaging extracts. Plasmids containing cDNA inserts

were excised from the recombinant lambda-Zap phage using

Ex-assist helper phage and propagated in SOLR cells."

Query Match 1.3%; Score 43.2; DB 2; Length 386;

Best Local Similarity 50.0%; Pred. No. 0.96;

Matches 108; Conservative 0; Mismatches 108; Indels 0; Gaps 0;

QY 1394 ATACAAGATTCTCAAGTAATAATAACAGGCAATCTTGATATCTCAACTGAGCTGGGAAT 1453

|||

Db 81 ATAGCATAAACCTAGCAATTAATGGTAAATGATTAATCTCACCTGGCTGTTAGGT 140

|||

QY 1454 GTCAACAACCTCGATCAAGTAATGCTTTGAATAGTTAGAGAAAGCAACAGAAAAGTAGAC 1513

|||

Db 141 GTAAACATCGTGGTCAAGAACACAATGAATGGTTCTCGAAGAGAGACAGAAAGAGAG 200

|||

QY 1514 AAGTCAATGTCAACTGACTAGACATCTGCTCTCTATTACCTATATCTGTTTGACTATC 1573

|||

Db 201 AGATCAAGTTTGTAATATATCTTCTTAACGGAAGCTTTGTAAGTTTGTGTTAAATC 260

|||

QY 1574 ATATCTCTGTTTGTGTATACCTAGCTGATCTTA 1609

|||

Db 261 ATACGTTTGAGTTTAGTTGCTTTTGGACTTTA 296

RESULT 7

AL380807

LOCUS

DEFINITION

AL380807

VERSION

AL380807.1

KEYWORDS

SOURCE

ORGANISM

Medicago truncatula (barrel medic)

Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;

Medicago.

1 (bases 1 to 494)

Journet, B.P., Crespeau, H., van Tuinen, D., Gouzy, J., Jaillon, O.,

Niebel, A., Carreau, V., Chatagnier, O., Kahn, D.,

Gianinazzi-Pearson, V. and Gamas, P.

Medicago truncatula ESTs from Sinorhizobium meliloti-induced root

JOURNAL
COMMENT

nodes
Unpublished (2000)
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Contact: Pascal Gamas and Etienne-Pascal Journet, Laboratoire de
Biologie Moleculaire des Relations Plantes-Microorganismes,
CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email:
Mt-est@toulouse.inra.fr Website:
http://sequence.toulouse.inra.fr/Mtruncatula.html).

Location/Qualifiers
1. 494
/organism="Medicago truncatula"
/mol_type="mRNA"
/cultivar="Jemalong"
/db_xref="taxon:3880"
/clone="MtBB54F09"
/tissue_type="symbiotic root nodules"
/dev_stages="harvested 4 days post inoculation with
Sinorhizobium meliloti"
/clone_lib="MtBB"
/note="Vector: pBluescript pSK; Site 1: EcoRI; Site 2:
XhoI; Plants were grown in an aeroponic chamber on
nitrogen-rich medium for 21 days. Three days before
inoculation with Sinorhizobium meliloti, the medium was
replaced by N-free medium. Root nodules (+ short adjacent
root segments) were harvested 4 days post inoculation.
cDNA was prepared from polyA+ enriched RNA. The cDNA was
directionally ligated into Uni-zap XR vector from
Stratagene and packaged using Gigapack Gold packaging
extracts. Plasmids containing cDNA inserts were
mass-excised from phage stocks using Exaestit helper phage
and propagated in SOLR cells. Clone ordering and
sequencing was performed by the Centre National de
Sequencage (Genoscope, Evry, France)."

FEATURES
source
1. 494
/organism="Medicago truncatula"
/mol_type="mRNA"
/db_xref="taxon:3880"
/clone="NF058C11IN"
/tissue_type="local and systemic leaves"
/dev_stages="mature"
/clone_lib="Insect herbivory"
/note="Vector: Lambda Zap; Library was produced from fully
expanded M. truncatula leaves of plants fed upon by
Spodoptera exigua (beet armyworm) for 24 hours. Systemic
(undamaged leaves from injured plants) and wounded leaves
were harvested and pooled."

ORIGIN
Query Match 1.3%; Score 43.2; DB 1; Length 494;
Best Local Similarity 50.0%; Pred. No. 1;
Matches 108; Conservative 0; Mismatches 108; Indels 0; Gaps 0;
Qy 1394 ATACAGATTCTCAAGTAATAATACAGGCAATCTTGATATCTCACTGACCTGGGAAT 1453
Db 190 ATAGCATAAACCCCTAGCAATATGCTGCTAAATGATATCTCACACGTCGCTGTAGGT 249
Qy 1454 GTCAACAACTCGATCAGTAATGCTTGAATAGTTAGAGGAAGCAACAGAAAAGTACGAC 1513
Db 250 GTAACATCGTGGTCAAGAACACATGAATGGTTCTCGAAGAGAGACAGAGAAGAGAG 309
Qy 1514 AAAGTCAATGTCAAACTGACTAGCACATCTGCTCTCATATCTATATCTATCTGTTTGGACTATC 1573
Db 310 AGATCAAGTTTGTAAATATCTCTTAACGGAGAAGCTTTGTAAAGTTTGTGGTGTAAATC 369
Qy 1574 ATATCTCTGTTTGGTATATCTAGCTGATTTCTTA 1609
Db 370 ATACGGTTTGAGTTAGTTTGGCTTTTGGGACTTTA 405

RESULT 8
BF641250/c
LOCUS
DEFINITION
BF641250.1 Insect herbivory Medicago truncatula cDNA clone
NF058C11IN 5', mRNA sequence.
ACCESSION
BF641250
VERSION
BF641250.1 GI:11905408
KEYWORDS
EST.
ORGANISM
Medicago truncatula (barrel medic)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 670)
Korth,K., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
Flores,H.R., Inman,J.T., Wellner,J.W. and May,G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula insect herbivory library
Unpublished (2000)
Contact: Korth K
Dept. of Plant Pathology
University of Arkansas
217 Plant Science Building, Fayetteville, AR 72701, USA
Tel: 501 575 5191
Fax: 501 575 7601
Email: kkorth@comp.uark.edu
Insert Length: 670 Std Error: 0.00
Plate: 058 row: C column: 11
Seq primer: TCACACAGAAACAGCTATGAC.
Location/Qualifiers
1. 670
/organism="Medicago truncatula"
/mol_type="mRNA"
/db_xref="taxon:3880"
/clone="NF058C11IN"
/tissue_type="local and systemic leaves"
/dev_stages="mature"
/clone_lib="Insect herbivory"
/note="Vector: Lambda Zap; Library was produced from fully
expanded M. truncatula leaves of plants fed upon by
Spodoptera exigua (beet armyworm) for 24 hours. Systemic
(undamaged leaves from injured plants) and wounded leaves
were harvested and pooled."

ORIGIN
Query Match 1.3%; Score 43.2; DB 2; Length 670;
Best Local Similarity 50.0%; Pred. No. 1.2;
Matches 108; Conservative 0; Mismatches 108; Indels 0; Gaps 0;
Qy 1394 ATACAGATTCTCAAGTAATAATACAGGCAATCTTGATATCTCACTGACCTGGGAAT 1453
Db 241 ATAGCATAAACCCCTAGCAATATGCTGCTAAATGATATCTCACACGTCGCTGTAGGT 182
Qy 1454 GTCAACAACTCGATCAGTAATGCTTGAATAGTTAGAGGAAGCAACAGAAAAGTACGAC 1513
Db 181 GTAACATCGTGGTCAAGAACACATGAATGGTTCTCGAAGAGAGACAGAGAAGAGAG 122
Qy 1514 AAAGTCAATGTCAAACTGACTAGCACATCTGCTCTCATATCTATCTGTTTGGACTATC 1573
Db 121 AGATCAAGTTTGTAAATATCTCTTAACGGAGAAGCTTTGTAAAGTTTGTGGTGTAAATC 62
Qy 1574 ATATCTCTGTTTGGTATATCTAGCTGATTTCTTA 1609
Db 61 ATACGGTTTGAGTTAGTTTGGCTTTTGGGACTTTA 26

RESULT 9
CNS03RIF/c
LOCUS
DEFINITION
CNS03RIF 1022 bp DNA linear GSS 01-SEP-2000
Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
049L07 of library G from Tetraodon nigroviridis, genomic survey
sequence.
AL257280
ACCESSION
VERSION
AL257280.1 GI:7978292
KEYWORDS
GSS; genome survey sequence.
SOURCE
Tetraodon nigroviridis
ORGANISM
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
1
Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Pizanes,C., Wincker,P., Brottier,P., Queirier,F.,
Saurin,W. and Weissenbach,J.
Estimate of human gene number provided by genome-wide analysis

REFERENCE
AUTHORS
TITLE

using Tetraodon nigroviridis DNA sequence

JOURNAL
MEDLINE
PUBMED

20296633
10835645

REFERENCE
AUTHORS

Roest Crolius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
Saurin,W., Bernot,A. and Weissenbach,J.
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis

JOURNAL
MEDLINE
PUBMED

20359837
10899143

REFERENCE
AUTHORS

3 (bases 1 to 1022)

TITLE
JOURNAL

Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segret@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/tetraodon.

FEATURES
source

1. .1022
/location/Qualifiers
/organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="049L07"
/clone_lib="G"
/note="Genoscope sequence ID : COBG049CF048P1-end ;
PUC-Ori"

ORIGIN

Query Match 1.3%; Score 42.6; DB 9; Length 1022;

Best Local Similarity 49.3%; Pred. No. 2.1;
Matches 111; Conservative 0; Mismatches 114; Indels 0; Gaps 0;

Qy 1360 GGAATTCGATCTACTATCAGAGAATATCTCAATACAGATTCTCAAGTAATAAAC 1419

Db 837 GGTATTAGATTACGGTACCAAAATTATTTCTATATGCTAAATGGCAAGTAATGAAG 778

Qy 1420 AGCAATCTTGATATCTCAATGAGCTTGGAGTGTCAACAACCTCGATCAAGTAATGCTTT 1479

Db 777 GAGAATCTGTATTATCTTCCCAAGAGTCAGAAGTTGCATACACTATTACTATGCTCTT 718

Qy 1480 GAATTAAGTTAGAAAGCAACAGAACTAGACAAAGTCAATGTCAACGTAGTAGCAC 1539

Db 717 AAACAAATTTGGGAAGCCCAAGTGATTATGTCACTACCTTGGAAATATTATTGAAAGTCTC 658

Qy 1540 ATCTGCTCTCATTACCTATATCGTTTGGACTATCATATCTCTGT 1584

Db 657 TGATAGTTTATTACCAATTTGGTTCATCTTTTCAACAATTAAT 613

RESULT 10
CD081007

LOCUS
CD081007
MA3-9999U-M317-D07-U.G MA3-0001 Schistosoma mansonii CDNA clone
MA3-9999U-M317-D07.G, mRNA sequence.

ACCESSION
VERSION

CD081007.1 GI:34632000

KEYWORDS
SOURCE

EST.

ORGANISM

Schistosoma mansonii

Schistosoma mansonii

Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;

Strigoida; Schistosomatidae; Schistosomatidae; Schistosoma.

1 (bases 1 to 507)

Verjovski-Almeida,S., DeMarco,R., Martins,E.A.L., Guimaraes,P.E.M.,

Ojopi,E.P.B., Paquola,A.C.M., Piazza,J.P., Nishiyama,M.Y. Jr.,

Kitajima,J.P., Adamson,R.E., Ashton,P.D., Bonaldo,M.F.,

Coulson,P.S., Dillon,G.P., Farias,L.P., Gregorio,S.P., Ho,P.L.,

Leite,R.A., Malaquias,L.C.C., Marques,R.C.P., Miyasato,P.A.,

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

Nascimento,A.L.T.O., Ohlweiler,F.P., Reis,E.M., Ribeiro,M.A.,

Sa,R.G., Stukart,G., Soares,M.B., Gargioni,C., Kawano,I.,

Rodrigues,V., Madeira,A.M.B.N., Wilson,R.A., Menck,C.F.M.,

Setubal,J.C., Leite,L.C.C. and Dias-Neto,E.

Transcriptome analysis of the acoelomate human parasite Schistosoma

mansonii

Nat. Genet. 35 (2), 148-157 (2003)

22879926

12973350

Contact: Dr. Sergio Verjovski-Almeida

Departamento de Bioquímica

Instituto de Química - Universidade de São Paulo

Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 São Paulo - SP,

Brasil

Tel: +55-11-3091-2173

Fax: +55-11-3091-2186

Email: verjo@iq.usp.br

This sequence was derived from the FAPESP Schistosoma mansonii EST

Genome Project. All sequences in the project were assembled and

annotated. This entry and all the assembled sequences can be seen

in the following URL http://bioinfo.iq.usp.br/schisto/

Plate: MA3-9999U-M317 row: 7 column: D.

FEATURES

Location/Qualifiers

1. .507

/organism="Schistosoma mansonii"

/mol_type="mRNA"

/db_xref="taxon:6183"

/clone="MA3-9999U-M317-D07.G"

/sex="mixed pool"

/dev_stage="adult"

/lab_host="Mus musculus"

/clone_lib="MA3-0001"

ORIGIN

Query Match 1.3%; Score 42.4; DB 6; Length 507;

Best Local Similarity 49.4%; Pred. No. 1.8;

Matches 88; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

Qy 1481 AATAAGTTAGAGAAAGCAAGAACTAGACAAAGTCAATGCTAAAGTACTAGCACA 1540

Db 130 AACAGTTTCCCAATACACACACACACACACCGTTATTAAAGCGTTACTAGCTAA 189

Qy 1541 TCCTGCTCTCATTAATACCTATATCGTTTGTGACTATCATATCTCTTGTGTTGTTATCTAGC 1600

Db 190 ACCTGTCATCATCGTTTATTCCTTGAATAATATTTCAGACATTTAATCGTCATTGGA 249

Qy 1601 CTGATTTAGCATGCTACCTAATGTACAGCAAGCGCACACAAAAACCTTATTAT 1658

Db 250 TCCAAATCTCATGTTTACCGATNNNNNNNNNNNNNNNNNNNAGCAATAAT 307

RESULT 11

BH183366/c

LOCUS

DEFINITION

023_G 14-21 SmBAC1 Schistosoma mansonii genomic clone 023G14 5',

genomic survey sequence.

ACCESSION

BH183366

VERSION

BH183366.1 GI:16288520

KEYWORDS

GSS.

SOURCE

Schistosoma mansonii

Schistosoma mansonii

Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;

Strigoida; Schistosomatidae; Schistosomatidae; Schistosoma.

1 (bases 1 to 816)

Le Paslier,M.C., Pierce,R.J., Merlin,F., Hirai,H., Wu,W.,

Williams,D.L., Johnston,D., Loverde,P.T. and Le Paslier,D.

Construction and characterization of a Schistosoma mansonii

baconian artificial chromosome library

Genomics 65 (2), 87-94 (2000)

20247247

10783255

Other_GSSs: 023_G 14-rev

Contact: Pierce_RJ

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